

GenCore version 5.1.3
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OK nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:33:27 : Search time 100 Seconds

(Without alignments)
15088,964 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268

Sequence: 1 cccaagaccacctcttcgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:

1: /cgn2_6/pdata/1/lna/5A.COMB.seq:

2: /cgn2_6/pdata/1/lna/2B.COMB.seq:

3: /cgn2_6/pdata/1/lna/3B.COMB.seq:

4: /cgn2_6/pdata/1/lna/6B.COMB.seq:

5: /cgn2_6/pdata/1/lna/PCUS.COMB.seq:

6: /cgn2_6/pdata/1/lna/backfiles1.seq:

Printed. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	0.8	3	2	US-08-451-822A-9
2	33	0.8	3	4	US-08-451-822A-9
3	33	0.8	3	1	US-08-451-822A-9
4	33	0.8	3	1	US-08-451-822A-9
5	33	0.8	3	1	US-08-451-822A-9
6	33	0.8	3	1	US-08-451-822A-9
7	33	0.8	3	1	US-08-451-822A-9
8	33	0.8	3	1	US-08-451-822A-9
9	33	0.8	3	1	US-08-451-822A-9
10	33	0.8	3	1	US-08-451-822A-9
11	33	0.8	3	1	US-08-451-822A-9
12	33	0.8	3	1	US-08-451-822A-9
13	33	0.8	3	1	US-08-451-822A-9
14	33	0.8	3	1	US-08-451-822A-9
15	33	0.8	3	1	US-08-451-822A-9
16	33	0.8	3	1	US-08-451-822A-9
17	33	0.8	3	1	US-08-451-822A-9
18	33	0.8	3	1	US-08-451-822A-9
19	33	0.8	3	1	US-08-451-822A-9
20	33	0.8	3	1	US-08-451-822A-9
21	33	0.8	3	1	US-08-451-822A-9
22	33	0.8	3	1	US-08-451-822A-9
23	33	0.8	3	1	US-08-451-822A-9
24	33	0.8	3	1	US-08-451-822A-9
25	33	0.8	3	1	US-08-451-822A-9
26	33	0.8	3	1	US-08-451-822A-9
27	33	0.8	3	1	US-08-451-822A-9

C 28	22	0.5	45	5	PCT-US93-03256-11	Sequence 11, Appl
C 29	21.8	0.5	37	4	US-09-526-542-19	Sequence 19, Appl
C 30	21.8	0.5	40	4	US-09-306-290-34	Sequence 34, Appl
C 31	21.8	0.5	43	2	US-08-686-599A-14	Sequence 14, Appl
C 32	21.8	0.5	44	1	US-09-103-356A-12	Sequence 12, Appl
C 33	21.8	0.5	44	4	US-09-672-039A-4	Sequence 4, Appl
C 34	21.4	0.5	25	2	US-08-672-039A-4	Sequence 2, Appl
C 35	21.2	0.5	38	4	US-09-454-704A-7	Sequence 7, Appl
C 36	21.2	0.5	42	3	US-08-757-024-16	Sequence 16, Appl
C 37	21.2	0.5	44	3	US-08-757-024-16	Sequence 15, Appl
C 38	21.2	0.5	43	3	US-08-757-024-14	Sequence 14, Appl
C 39	21.2	0.5	43	2	US-08-471-025-14	Sequence 14, Appl
C 40	21.2	0.5	46	3	US-08-757-024-13	Sequence 13, Appl
C 41	21.2	0.5	46	3	US-08-757-024-11	Sequence 11, Appl
C 42	21.2	0.5	47	3	US-08-757-024-11	Sequence 10, Appl
C 43	21.2	0.5	48	3	US-08-757-024-10	Sequence 9, Appl
C 44	21.2	0.5	50	3	US-08-757-024-9	Sequence 8, Appl
C 45	21.2	0.5	50	3	US-08-757-024-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-451-822A-9/c
Sequence 9, Application US/08451822A
Patent No. 5863888
ORIGINAL INVENTOR:
APPLICANT: Dionne, Craig A
APPLICANT: Crumley, Greg G
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
ADDRESS: 500 Arcola Road
STREET: 500 Arcola Road
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPILED BY: PC DOS/MS-DOS
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08451.822A
FILING DATE: 26-MAY-1995
PRIORITY DATE: 26-MAY-1995
PRIORITY APPLICATION: 043
APPLICATION NUMBER: US 08/223,430
FILING DATE: 14-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A0496E
TELEPHONE: (610) 244-3816
TELEFAX: (610) 244-3808
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDNESS: single
MOLECULE TYPE: cDNA

US-08-451-822A-9

Query Match 0.8%; Score 33; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2707 TATCCACACATTAACGGCAGCTTTAAACATCA 2739

Db 33 TATCCACACATTAACGGCAGCTTTAAACATCA 1

RESULT 2
US-08-323-430-9/C

Sequence 2, Application US/08323430

Sequence 2, Application US/08323430

GENERAL INFORMATION:

APPLICANT: Diomed, Craig A

APPLICANT: Crumley, Greg

APPLICANT: Jave, Michael C

APPLICANT: Schlessinger, Joseph

TITLE OF INVENTION: Fibroblast Growth Factor Receptors

CORRESPONDENCE ADDRESS:

STREET: 500 Arcola Road

CITY: Collegeville

STATE: PA USA

COUNTRY: PA USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 05/08/323.430

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US to be assigned

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: US 07/549,587

ATTORNEY/AGENT INFORMATION:

NAME: Goodman, Rosanne

REGISTRATION NUMBER: 32,534

REFERENCE/DOCKET NUMBER: A0496

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 454-3817

TELEFAX: (215) 454-3808

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-323-430-9

Query Match 0.8%; Score 33; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2707 TATCCACACATTAACGGCAGCTTTAAACATCA 2739

Db 33 TATCCACACATTAACGGCAGCTTTAAACATCA 1

RESULT 3

US-08-471-570-15/C

Sequence 15, Application US/08471570

Patent No. 5750371

GENERAL INFORMATION:

APPLICANT: IGARASHI, KOICHI

APPLICANT: SENOO, Masaharu

APPLICANT: MATSUNABE, Tetsuya

TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESS: DAVID G. COLLIN; DIKE, BRONSTEIN, ROBERTS &

STREET: 130 Water Street

CITY: Boston

STATE: Massachusetts

COUNTRY: US

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/471,570

FILING DATE:

APPLICATION NUMBER: US 07/743369

FILING DATE: 16-AUG-1991

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 29822

REFERENCE/DOCKET NUMBER: 40897

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)523-3400

TELEFAX: (617)523-6440

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid, synthetic DNA

US-08-471-570-15

Query Match 0.8%; Score 33; DB 1; Length 39;

Best Local Similarity 84.6%; Pred. No. 28;

Matches 33; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1873 GAGATGACATGATGATGATGGAACCAACAAAT 1911

Db 39 GAGATGACATGATGATGATGGAACCAACAAAT 1

RESULT 4

US-07-947-683-15/C

Sequence 15, Application US/07947683

Patent No. 5589451

GENERAL INFORMATION:

APPLICANT: STEVEN E

TITLE OF INVENTION: METHODS AND TREATMENTS FOR

TITLE OF INVENTION: CORNEAL HEALING WITH HEPATOCYTE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: ARNOLD, WHITE & DUKKEE

STREET: 100 BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

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? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WORDPERFECT 5.1
? CURRENT RELEASE DATE: 05/07/94/7 693
? APPLICATION NUMBER: 07/94/7 693
? FILING DATE: SEPTEMBER 21, 1992
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
? NAME: KITCHELL, BARBARA S.
? REGISTRATION NUMBER: 33,928
? REFERENCE/DOCKET NUMBER: UTSD-311/KIT
? TELEPHONE: 512-320-7200
? TELEFAX: 512-474-7577
? TELEX: NOT APPLICABLE
? INFORMATION FOR SEQ ID NO: 15:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 30 base pairs
? TOPOLOGY: single
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-07-947-693-15

Query Match 0.7%: Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1;e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1242 GATTGAGGTTCTCTATATCGAATGTAC 1271
DB 30 GATTGAGGTTCTCTATATCGAATGTAC 1

RESULT 5
US-08-400-323-18/c
? Sequence 18, Application US/08400323
? Patent No. 5703047
? GENERAL INFORMATION:
? APPLICANT: Wilson, Steven E.
? TITLE OF INVENTION: Methods and Treatments for Corneal
? TYPE OF INVENTION: Healing with Growth Factors
? CORRESPONDENCE ADDRESS:
? ADDRESSES: Arnold, Millic 6 Durkee
? STREET: P. O. Box 4433
? CITY: Houston
? STATE: TX
? COUNTRY: USA
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? FILING DATE: 05/08/400,323
? CLASSIFICATION: 514
? ATTORNEY/AGENT INFORMATION:
? NAME: Kitchell, Barbara S.
? REGISTRATION NUMBER: 33,928
? REFERENCE/DOCKET NUMBER: UTSD-431/KIT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 512-474-7577
? TELEFAX: 512-474-7577
? TELEX: 79-0924
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 30 base pairs
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-400-323-18

Query Match 0.7%: Score 30; DB 1; Length 30;

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? Best Local Similarity 100.0%; Pred. No. 1;3e+02;
? Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1242 GATTGAGGTTCTCTATATCGAATGTAC 1271
DB 30 GATTGAGGTTCTCTATATCGAATGTAC 1

RESULT 6
US-07-997-133-4/c
? Sequence 4, Application US/07997133
? Patent No. 5288855
? GENERAL INFORMATION:
? APPLICANT: Betgonzoul, Laura
? APPLICANT: Masque, Guy
? APPLICANT: Isaacchi, Antonella
? APPLICANT: Ronuccci, Romeo
? APPLICANT: Samlientos, Paolo
? TITLE OF INVENTION: Extracellular Form of the Human
? TYPE OF INVENTION: Fibroblast Growth Factor Receptor
? CORRESPONDENCE ADDRESS:
? ADDRESSES: OBILON, SPIVAK, MCCLELLAND, MATER & NEUBADT,
? STREET: 1755 Jefferson Davis Highway, Fourth Floor
? CITY: Arlington
? STATE: Virginia
? COUNTRY: USA
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? FILING DATE: 05/07/997,133
? CLASSIFICATION: 510
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/642,755
? FILING DATE: 18-JAN-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: OBILON, NO. 5288855man F.
? REGISTRATION NUMBER: 24,618
? REFERENCE/DOCKET NUMBER: 695-226-0
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)521-4500
? TELEFAX: (703)486-2347
? TELEX: 248855 OPAT UR
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 30 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: unknown
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? US-07-997-133-4

Query Match 0.6%: Score 25.8; DB 1;
Best Local Similarity 93.1%; Pred. No. 1;5e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2488 TCTTGCGATCGAGTGCCCTCCGACGAGACC 2516
DB 30 TCTTGCGATCGAGTGCCCTCCGACGAGACC 2

RESULT 7
US-07-997-133-4/c
? Sequence 4, Application US/07997133
? GENERAL INFORMATION:
? APPLICANT: Betgonzoul, Laura
? APPLICANT: Masque, Guy
? APPLICANT: Isaacchi, Antonella

```

APPLICANT: BENCUCU, Romeo
APPLICANT: Sacramento, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Fibroblast Growth Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: OGDON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/997,133
FILING DATE: 28-DEC-1992
CLASSIFICATION: D530
PRIORITY NUMBER: 0530
APPLICATION NUMBER: 18-JAN-1991
FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 769-226-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)1486-2347
TELEFAX: 248655 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-997-133-4
Query Match 0.6%; Score 25.8; DB 5; Length 30;
Best Local Similarity 93.1%; Pred. No. 1.5e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Cy 2488 TCTTGCGATCGATCGCTCCGACGAGACC 2516
Db 30 TCTTGCGATCGATCGCTCCGACGAGACC 2

RESULT 9
US-08-859-998-431
Sequence 431, Application US/08859998
Patent No. 5594076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jorkhize, George
APPLICANT: Jorkhize, George
TITLE OF INVENTION: A METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
TELEPHONE: 415-322-5070
TELEFAX: 415-322-5070
INFORMATION FOR SEQ ID NO: 432:
SEQUENCE CHARACTERISTICS:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 03096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-322-5070
INFORMATION FOR SEQ ID NO: 431:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-431
Query Match 0.6%; Score 25; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 768 GCTCATGCTGCTGCTGCGGCGAC 792
Db 1 GCTCATGCTGCTGCTGCGGCGAC 25

RESULT 9
US-08-859-998-432/C
Sequence 432, Application US/08859998
Patent No. 5594076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jorkhize, George
APPLICANT: Bidlishvili, Robert
TITLE OF INVENTION: A METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
TELEPHONE: 415-322-5070
TELEFAX: 415-322-5070
INFORMATION FOR SEQ ID NO: 432:
SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-09-954-998-432
Query Match 0.6% Score 25 DB 2 Length 25
Best Local Similarity 100.0% Pred. No. 2.le+03
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 25 GCGCCAGCGGCTGCCCTACTCAAG 1
RESULT 10
US-09-225-928-431
Sequence 431, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Biblishvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
FAX: 415-322-5075
INFORMATION FOR SEQ ID NO: 431:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 431:
US-09-225-928-431
Query Match 0.6% Score 25 DB 4 Length 25;
Best Local Similarity 100.0% Pred. No. 2.le+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
768 GCGTCATCGTGGCGCGGCGCAAC 792
|||||

Db 1 GCGTCATCGTGGCGCGGCGCAAC 25
RESULT 11
US-09-225-928-432/c
Sequence 432, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Biblishvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-May-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
FAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 432:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 432:
US-09-225-928-432
Query Match 0.6% Score 25 DB 4 Length 25;
Best Local Similarity 100.0% Pred. No. 2.le+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 25 GCGCCAGCGGCTGCCCTACTCAAG 1
RESULT 12
US-08-451-822A-10
Sequence 10, Application US/08451822A
Patent No. 6563888
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
Crumley, Greg
APPLICANT: Jaye, Michael C
Schlesinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

```

ADDRESS: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
STATE: PA
COUNTRY: USA
TELEPHONE: (610) 454-3816
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 56408/451.822A
PRIORITY: 56408/451.1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/323,430
FILING DATE: 14-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 14-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 28,699
REFERENCE/DOCKET NUMBER: A0496E
TECHNOLOGY/INVENTION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-451-822A-10

Query Match 0.6%; Score 25; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Cy 271 ACCTGCTGCACTGCGTCTGCTTCA 295
Db 21 ACCTGCTGCACTGCGTCTGCTTCA 45

RESULT 13
US-08-323-430-10
Sequence 10: Application US/08323430
Patent No. 6,446
GENERAL INFORMATION:
APPLICANT: Dione, Craig A
APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Schlassefinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```

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1 APPLICATION NUMBER: US/08/323,430
2 FILING DATE:
3 PRIORITY APPLICATION: 435
4 PRIORITY APPLICATION DATA: US to be assigned
5 APPLICATION NUMBER: US to be assigned
6 FILING DATE: 21-AUG-1992
7 APPLICATION NUMBER: US 07/549,587
8 FILING DATE: 06-JUL-1990
9 ATTORNEY/AGENT INFORMATION:
10 NAME: Goodman, Rosanne
11 REGISTRATION NUMBER: 32,534
12 REFERENCE/DOCKET NUMBER: A0496
13 TELEPHONE/DOCKET NUMBER:
14 TELEPHONE: (215) 454-3817
15 TELEFAX: (215) 454-3808
16 INFORMATION FOR SEQ ID NO: 10:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 45 base pairs
19 TYPE: nucleic acid
20 STRANDEDNESS: single
21 TOPOLOGY: linear
22 MOLECULE TYPE: cDNA
23 US-08-323-430-10
24
25 Query Match 0.6%; Score 25; DB 4; Length 45;
26 Best Local Similarity 100.0%; Pied.No. 2,7e+03;
27 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
28
29 Qy 271 ACACATGCTACGCTGCGTCTTCA 295
30 | | | | | | | | | | | | | | | | | |
31 Db 21 ACATGCTACGCTGCGTCTTCA 45
32
33 RESULT 14
34 US-08-371-001-4
35
36 Patent No. 5,781,663
37 Patent No. 5,781,663
38 GENERAL INFORMATION:
39 APPLICANT: Morrison Ph.D., Richard
40 TITLE OF INVENTION: Methods and Composition for Treating
41 TITLE OF INVENTION: Tumor Cells
42 NUMBER OF SEQUENCES: 14
43 CORRESPONDENCE ADDRESS:
44 ADDRESSEE: Dr. J. Hargis & Friedmannrich
45 STREET: 4011 S.
46 CITY: San Diego
47 STATE: CA
48 COUNTRY: USA
49 ZIP: 92101
50
51 COMPUTER READABLE FORM:
52 MEDIUM TYPE: floppy disk
53 OPERATING SYSTEM: PC-DOS/MS-DOS
54 SOFTWARE: Patentin Release #1.0, Version #1.25
55 CURRENT APPLICATION DATA:
56 APPLICATION NUMBER: US/08/371,001
57 FILING DATE: January 10, 1995
58 CLASSIFICATION: 435
59 ATTORNEY/AGENT INFORMATION:
60 NAME: Goodman, Rosanne
61 REGISTRATION NUMBER: 32,534
62 REFERENCE/DOCKET NUMBER: A0496
63 TELEPHONE/DOCKET NUMBER: P00095050
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: (619) 699-3630
66 TELEFAX: (619) 236-1048
67 INFORMATION FOR SEQ ID NO: 4:
68 SEQUENCE CHARACTERISTICS:
69 LENGTH: 45 base pairs
70 TYPE: nucleic acid
71 STRANDEDNESS: single
72 TOPOLOGY: linear
73 MOLECULE TYPE: Other Nucleic Acid
74 US-08-371-001-4

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Query Match 0.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 207 AACGTCTCAGATGGATTAACGTC 230
 |||||||||||||||||||||
 DB 1 AACGTCTCAGATGGATTAACGTC 24

RESULT 15
 US-08-451-822A-11/C
 ; Sequence 11, Application US/08451822A
 ; Patent No. 5863888
 ; GENERAL INFORMATION:
 ; APPLICANT: Dionne, Craig A
 ; APPLICANT: Grunley, Greg
 ; APPLICANT: Jey, Michael C
 ; APPLICANT: Krasinsinger, Joseph
 ; TITLE OF INVENTION: Humanolest Growth Factor Receptors
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
 ; STREET: 500 Arcola Road
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: In release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/451,822A
 ; FILING DATE: 26-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; PRIORITY APPLICATION NUMBER: US 08/323,430
 ; FILING DATE: 11-SEP-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/934,372
 ; FILING DATE: 21-AUG-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/549,587
 ; FILING DATE: 06-JUL-1990
 ; ATTORNEY/CONS. INFORMATION:
 ; NAME: Smith, Mark L.
 ; REGISTRATION NUMBER: 29,659
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3816
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 11:
 ; DEFINITION: HUMANOLEST GROWTH FACTOR
 ; LENGTH: 24 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-451-822A-11

Query Match 0.6%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 503 TGCACTTGGGGCCCAACATAGGA 526
 |||||||||||||||||||||
 DB 24 TGCACTTGGGGCCCAACATAGGA 1

Search completed: December 11, 2002, 17:47:48
 Job time : 105 secs

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GenCore version 5.1.3
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OW nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:31:33 : Search time 551 Seconds

(Without alignments)
1743.791 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268
Sequence: 1 cccaagaccactcttcgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY-MQC
Gapox 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32	0.7	32	13	AA023618
C 2	30	0.7	30	18	AA063287
C 3	30	0.7	30	19	AA055503
C 4	25	0.6	30	12	AA029597
C 5	25	0.6	30	22	AA023509
C 6	25	0.6	25	24	AA065344
C 7	25	0.6	42	20	AA084630
C 8	25	0.6	45	13	AA023619
C 9	25	0.6	45	13	AA023619

C 10	24.8	0.6	49	23	AA129254	Human SNP oligonuc
C 11	24.6	0.6	31	22	AA130470	Human single nucleic
C 12	24.6	0.6	50	21	AA083316	Human NSIB fragment
C 13	24.4	0.6	42	16	AA070596	D101 linked oligon
C 14	24.2	0.6	47	20	AA032549	Human genome b1a11
C 15	24.2	0.6	47	21	AA026594	Human map-related
C 16	24.2	0.6	32	13	AA071050	Be1aB - a PCR prime
C 17	24	0.6	45	23	AA071050	Human SNP oligonuc
C 18	24	0.6	24	17	AA071050	Human SNP oligonuc
C 19	23.6	0.6	45	22	AA028218	Human genome b1a11
C 20	23.6	0.6	37	22	AA058623	Murine c-KIT exon
C 21	23.6	0.6	47	21	AA046611	AV rich sequence 1
C 22	23.6	0.6	49	24	AA075039	Human ACT wt cDNA
C 23	23.6	0.6	50	22	AA028400	Human ACT wt cDNA
C 24	23.4	0.5	40	22	AA071050	Human stRNA p41 gen
C 25	23.4	0.5	46	24	AA059573	Alu element
C 26	23.4	0.5	47	23	AA086884	CNS disorder-relat
C 27	23	0.5	31	22	AA013049	Human single nucle
C 28	23	0.5	44	22	AA030410	Human SNP oligonuc
C 29	23	0.5	44	22	AA030581	Human SNP oligonuc
C 30	22.6	0.5	43	20	AA046529	Human SNP oligonuc
C 31	22.6	0.5	41	22	AA071050	Human SNP oligonuc
C 32	22.6	0.5	46	22	AA028455	Human genome b1a11
C 33	22.6	0.5	47	20	AA032599	Human genome b1a11
C 34	22.6	0.5	48	8	AA071061	5'-3' probe for ex
C 35	22.6	0.5	49	19	AA071447	Nucleotide sequenc
C 36	22.6	0.5	49	22	AA098419	Human cDNA clone B
C 37	22.6	0.5	50	15	AA066822	Poly-da 50mer prob
C 38	22.6	0.5	50	15	AA066822	Conjugate forming
C 39	22.6	0.5	50	24	AA080897	CDNA #1012 encodin
C 40	22.6	0.5	50	24	AA080897	Mouse b2P4 receptor
C 41	22.4	0.5	28	19	AA044045	Human SNP oligonuc
C 42	22.4	0.5	42	28	AA031043	Human SNP oligonuc
C 43	22.4	0.5	46	24	AA053731	Allele discriminat
C 44	22.4	0.5	47	21	AA053731	Human map-related
C 45	22.2	0.5	50	22	AA029037	Human SNP oligonuc

ALIGNMENTS

RESULT 1
AA023618/c
AA023618 standard, DNN, 32 BP.
ID AA023618:
AC AA023618:
GT 21-MAY-1992 (first entry)
DT 3' embk - a bak probe.
RX Bacterially expressed kinase: CTS-1;
RW PCDF, tyrosine kinase: ss.
OS Synthetic.
XX W09200999-A.
XX 23-JAN-1992.
XX 03-JUL-1991: 91WO-US04745.
XX 06-JUL-1990: 90US-0549587.
XX (ROSE) RORER INT HOLDINGS.
XX Dloune CA, Crumley G, Jaje MC, Schlessinger J;
XX WPI: 1992-056827/07.
XX P-PSDB: AAR20750.
XX New fibroblast growth factor receptor proteins - useful in
XX treating of mediated conditions e.g. angiogenesis of tumours,
XX PT


```

XX 05-JAN-1999: 99US-0225928.
XX
XX 21-MAY-1997: 97US-085998.
XX
XX (CLON-) CLONTECH LAB INC.
XX
XX Chenchik A, Johhadze G, Bibilashvili R:
XX WPI: 2002-314699/35.
XX
XX Producing sub-population of labeled nucleic acids, useful for analysing
XX differences in RNA profiles between several different physiological
XX sources, using set of distinct gene specific primers
XX
XX Example 3: SEQ ID NO 431: 11pp: English.
XX
XX The invention relates to producing a sub-population of labeled nucleic
XX acids (NAs) comprising contacting a NA sample from a physiological
XX source, with a pool of 50 distinct gene specific primers under suitable
XX conditions to enzymatically generate sub-population of NAs, where
XX each gene specific primer has a sequence complementary to a distinct
XX RNA gene and each labeled NA is generated using a single gene specific
XX primer. The method is useful for producing a sub-population of labeled
XX NAs which is useful for analysing the differences in the RNA profiles
XX between several different physiological sources, where the method
XX comprises producing subpopulation of labeled NAs for the different
XX physiological sources, comprising the populations for each physiological
XX source to identify differences between the populations where the comparison
XX is preferably performed by hybridising the labeled NAs for each of the
XX distinct physiological sources to an array of probe NAs stably
XX associated with the surface of a substrate to produce a hybridisation
XX pattern for each of the sources, and comparing the patterns for each of
XX the sources, where differential gene expression assays are normal
XX utilised in differential expression analysis of diseased or normal
XX tissue e.g. neoplastic a normal tissue or tissue of a different tissue or
XX diseased tissue types. The present sequence is a human gene specific PCR
XX primer used in the method of the invention.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from USPTO at
XX http://wipo.segdata.uspto.gov/sequence.html?DocID=635282981.
XX
XX Sequence 25 BP: 3 A: 10 C: 7 G: 5 T: 0 other:
XX
XX Query Match 0.6%: Score 25; DB 24; Length 25;
XX Best Local Similarity 100.0%; Prod. No. 1.4e+04;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 768 CCTCATGCTGTGCTGCGCCAC 792
XX DB 1 CCTCATGCTGTGCTGCGCCAC 25
XX
XX RESULT 7
XX AAK6344/C
XX ID AAK6344 standard; DNA: 25 BP.
XX
XX AAK6344;
XX
XX 02-JUL-2002 (first entry)
XX
XX Human gene specific PCR primer #432.
XX
XX Primer: ss: DNA microarray; differential expression analysis; human.
XX
XX Homo sapiens.
XX
XX OS
XX PN US6352829-B1.
XX
XX 05-MAR-2002.
XX
XX 05-JAN-1999: 99US-0225928.

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XX 21-MAY-1997: 97US-085998.
XX
XX (CLON-) CLONTECH LAB INC.
XX
XX Chenchik A, Johhadze G, Bibilashvili R:
XX WPI: 2002-314699/35.
XX
XX Producing sub-population of labeled nucleic acids, useful for analysing
XX differences in RNA profiles between several different physiological
XX sources, using set of distinct gene specific primers
XX
XX Example 3: SEQ ID NO 432: 11pp: English.
XX
XX The invention relates to producing a sub-population of labeled nucleic
XX acids (NAs) comprising contacting a NA sample from a physiological
XX source, with a pool of 50 distinct gene specific primers under suitable
XX conditions to enzymatically generate subpopulation complementary to a distinct
XX RNA gene and each labeled NA is generated using a single gene specific
XX primer. The method is useful for producing a sub-population of labeled
XX NAs which is useful for analysing the differences in the RNA profiles
XX between several different physiological sources, where the method
XX comprises producing subpopulation of labeled NAs for the different
XX physiological sources, comprising the populations for each physiological
XX source to identify differences between the populations where the comparison
XX is preferably performed by hybridising the labeled NAs for each of the
XX distinct physiological sources to an array of probe NAs stably
XX associated with the surface of a substrate to produce a hybridisation
XX pattern for each of the sources, and comparing the patterns for each of
XX the sources, where differential gene expression assays are normal
XX utilised in differential expression analysis of diseased or normal
XX tissue e.g. neoplastic a normal tissue or tissue of a different tissue or
XX diseased tissue types. The present sequence is a human gene specific PCR
XX primer used in the method of the invention.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from USPTO at
XX http://wipo.segdata.uspto.gov/sequence.html?DocID=635282981.
XX
XX Sequence 25 BP: 3 A: 7 C: 11 G: 4 T: 0 other:
XX
XX Query Match 0.6%: Score 29; DB 24; Length 25;
XX Best Local Similarity 100.0%; Prod. No. 1.4e+04;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 1179 GCGGACGGCGCCGCTCCAGC 1203
XX DB 25 GCGGACGGCGCCGCTCCAGC 1
XX
XX RESULT 8
XX AAX84630
XX ID AAX84630 standard; DNA: 42 BP.
XX
XX AAX84630;
XX
XX 16-SEP-1999 (first entry)
XX
XX Oligomer used in DNA obstruction assay.
XX
XX DNA obstruction assay; receptor interaction; ligand interaction;
XX biological sample characterization; diagnosis; diabetes; heart disease;
XX infectious disease; inflammatory disease; neoplastic disorder;
XX autoimmune disease; central nervous system disorder; ss.
XX
XX OS
XX PN WO9931267-A1.
XX
XX 24-JUN-1999.

```


xx PS Claim 1: Page 2088; 4143pp; English.

xx CC The present invention relates to oligonucleotides encoding polymorphic

xx CC proteins of proteins related to amylases, amyloid proteins, angiotensin,

xx CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

xx CC histones, kinases, colony stimulating factors, complement related

xx CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,

xx CC G-protein coupled receptors and thioesterases. The present sequence is

xx CC one such oligonucleotide. The oligonucleotides and the peptides encoded

xx CC by them may be used in the prevention or treatment of the diseases listed

xx CC above as disorders that may be prevented, diagnosed and/or treated include

xx CC multifactorial diseases with a genetic component, such as autoimmune

xx CC systems (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

xx CC systemic lupus erythematosus and Grave's disease), inflammation, cancer

xx CC (e.g. cancers of the bladder, brain, breast, colon and kidney,

xx CC leukaemia), diseases of the nervous system and an infection of pathogenic

xx CC organisms.

xx SO

xx Sequence 49 BP; 3 A; 3 C; 4 G; 3 T; 0 other:

XX

XX Query Match 0.6%; Score 24.8; DB 22; Length 49;

XX Best Local Similarity 72.7%; Pred. No. 2, 2e-04;

XX Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0.

Oy 4225 ACAGCACAATATGTCACCGAACTTAAAAAAAAAAAAA 4268

Db 49 AATTAAACAATAATCGCCCAAAAAAAAAAAAAAAAAAAAA 6

RESULT 11

AA130470

ID AA130470 standard; DNA: 31 BP.

AX AA130470:

XX

DT 18-OCT-2001 (first entry)

XX

DE Human single nucleotide polymorphism (SNP) rs6933 2.

XX

DE Human: resequencing: genotype: disease: forensic: paternity testing:

KM Human single nucleotide polymorphism; SNP; ss.

XX

CS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Variation replace(15,c)

FT /tag_a

FT /standard_name= "single nucleotide polymorphism"

WT W0200166800-AZ.

PX

PD 13-SEP-2001.

PF 07-MAR-2001: 2001WO-US07268.

XX

XX 07-MAR-2000: 2000US-0187510.

XX 22-MAR-2000: 2000US-0206125.

PA (WHD) WHITEHEAD INST BIOMEDICAL RES.

PI Cargill M, Ireland JS, Lander ES.

XX

WP1: 2001-522952/57.

XX

XX Nucleic acid molecules from the human genome which include polymorphic

XX sites useful in methods for predicting the presence, absence or

XX severity of a particular phenotype or disorder (e.g. diabetes)

XX associated with a particular genotype -

PS Claim 1: Page 87; 145pp; English.

XX

CC	The invention relates to the identification of nucleic acid molecules
CC	(AA129513-AA131114) from the human genome which include polymorphic sites
CC	which can predispose individuals to disease. Various genes from a number
CC	of individuals were resequenced and single nucleotide polymorphisms (SNPs)
CC	in these genes discovered. The invention provides a method for predicting the
CC	presence, associated with a particular phenotype or disorder (e.g.,
CC	containing the polymorphic sites may be useful in forensics and paternity
CC	testing.
XX	
XX	Sequence 31 BP; 3 A; 13 C; 12 G; 3 T; 0 other:
XX	
XX	Query Match 0 6% Score 24.6; DB 22;
XX	Base Local Similarity 87.1% Pred. No. 1,9e+04;
XX	Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db	1 ACGGAGCCATCTCTCCAAACCGGAGCTGACCCG 31
AA098316	AA
RESULT 12	
1D	AAA098316 standard; DNA; 30 BP.
AC	AAA98316;
XX	02-FEB-2001 (first entry)
DE	Human MSH6 fragment 8/exon 8 to 10 DNA Ref-Seq fragment 13.
KW	Human mismatch repair gene; MSH6; disease predisposition; genotype;
KW	multicell; carcinoma; colorectal; endometrial; ovarian; leukemia;
KW	neoplastic disease; drug development; ds.
XX	
XX	Homo sapiens.
XX	
XX	DE19909878-A1.
PN	07-SEP-2000.
PD	06-MAR-1999; 990E-1009878.
XX	
PR	06-MAR-1999; 990E-1009878.
XX	(UYDE) UNIV DRESDEN TECH.
PA	Plaschke J, Kruppa C, Schackert H;
PL	WPL; 2000-588378/56.
XX	
XX	Disclosure: Fig 3; 14pp; German.
XX	
XX	This invention describes a novel method of determining a predisposition
XX	to disease by genotyping a subject's DNA sequence (A) of the human
XX	mismatch repair gene, MSH6 at specified positions and comparing with
XX	reference DNA sequences, optionally taking into account all possible
XX	combinations of variations of the individual mutations, including any
XX	chosen absolute number of variations. (A), and analysis of their position
XX	sequences, are useful for the following: (i) determining an individual's
XX	to disease, especially colorectal, breast mutation rate (frequency of base
XX	substitutions, insertions and/or deletions) in ex vivo cells (e.g. carcinoma and
XX	predicting the progression, severity and survival time of patients with
XX	neoplastic disease; (iv) the development of therapeutic and "life-style"
XX	drugs; (v) predicting individual differences in response to known
XX	chemotherapeutic agents (e.g., cis-platin) or drugs developed from (iv);
XX	(vi) optimizing individual treatments and interventions in vivo cells, in
XX	neoplasia; (vii) controlling and intervening in neoplastic cells, in
XX	vivo or in vitro. (viii) constructing genes and vectors, particularly for

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:33:27 ; Search time 7153 Seconds

(without alignments)
17364,850 Million cell updates/sec

Title: US-09-954-556-3

Sequence: 1 cccaagccaccccttcgc.....acttaaaaaaaaaaaaaa 4268

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: *
1: gb_ba:*
2: gb_lig:*
3: gb_10:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_sts:*
10: gb_sy:*
11: gb_un:*
12: gb_vl:*
13: gb_yi:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO	Score	Query Match	Length	DB ID	Description
1	4268	100.0	4268	AX332811	AX332811 Sequence
2	4268	100.0	4268	AX334117	AX334117 Sequence
3	4268	100.0	4268	AX336422	AX336422 Sequence
4	4268	100.0	4268	HWK5SM1	M87770 Human fibro
5	3286	79.3	3315	HSTGFRB	X53832 Human bek m
6	3286	79.3	3315	HSTGFRB	X53832 Human bek m
7	3247	76.0	3248	HSTGFR2M	Z66641 H.sapiens f
8	3247	76.0	3248	HSTGFR2M	Z66641 H.sapiens f
9	2781	65.2	3106	HWK5FRA	M86534 Human testis
10	2670	62.6	3244	AX329662	AX329662 Sequence
11	2670	62.6	3244	HWK5SM111	M87125 Human secre
12	2672	61.9	3809	AF211257	AF211257 Canis fam
13	2672	61.9	3809	AF211257	AF211257 Canis fam
14	2672	61.9	3809	HWK5FRA	M87125 Human secre
15	2437	57.1	2481	HWK5FRA	M87125 Human secre
16	2404	56.3	2923	AB030077	AB030077 Homo sapi
17	2399	56.2	2826	AB030077	AB030077 Homo sapi
18	2397	56.2	3071	AB030075	AB030075 Homo sapi
19	2397	56.2	3071	AB030075	AB030075 Homo sapi
20	2397	56.2	3071	AB030075	AB030075 Homo sapi
21	2397	56.2	3071	AB030075	AB030075 Homo sapi
22	2310	54.1	3106	AB030073	AB030073 Homo sapi
23	2202	51.6	3120	HWK5FRA	M87125 Human secre
24	2191	51.3	2650	HWK5FRA	M87125 Human secre
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26	1977	46.3	2373	AF184968	AF184968 Oryctolag
27	1886	44.5	2111	BTGFR2M	Z68150 B. taurus mr
28	1886	44.5	2111	BTGFR2M	Z68150 B. taurus mr
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30	1828	42.8	2716	CHRCR2	X53131 Human bfr m
31	1817	42.6	1954	AR007158	AR007158 Sequence
32	1728	40.5	3037	MUSKGRF	M63503 Mouse kerat
33	1692	39.7	2310	AR007160	AR007160 Sequence
34	1687	39.5	2621	GGEX	X61992 G.gallus mr
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38	1660	38.9	126467	AF487553	AF487553 Homo sapi
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42	1367	32.0	2675	NV12FR	X74332 P. walli mn
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44	1330	31.0	3102	AR007135	AR007135 Sequence
45	1318	30.9	1603	AR007157	X53543 X. laevis mr

ALIGNMENTS

RESULT 1
LOCUS AX332811
DEFINITION Sequence 3320 from Patent WO946329.
ACCESSION AX332811
VERSION AX332811.1
KEYWORDS GI:18123445
SOURCE
ORGANISM Homo sapiens
Human
Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Young P.E., Augustus M., Carter K.C., Emmer R., Endress G.,
Hortigan S., Soppet D.R. and Weaver Z.
cancer gene determination and therapeutic screening using signature

Pred. No. is the number of results predicted by chance to have a

J00HNL gene seqs
 Patent: WO 0194629-A, 3.320.13-DEC-2001;
 Avalon Pharmaceuticals (US)
 Location/Qualifiers
 FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 1199 a 964 c 1028 g 1077 t
 ORIGIN

Query Match 100.0% Score 4268 Db 6; Length 4268;
 Best Local Similarity 100.0%; Mismatches 0;
 Matches 4268; Conservative 0; PidentMatches 0; Indels 0; Gaps 0;

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61 TCCATCCCAACCCAGCGGGGGCGGGGACACACACAGTCCCGAGACGCTTGCCATTC 120
 Db 61 TCCATCCCAACCCAGCGGGGGCGGGGACACACACAGTCCCGAGACGCTTGCCATTC 120

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 Db 301 CTGGCTGCTGCTACACATGCGACCTCTGCTGGGCGGCGGCTCTTCAGATTGTTGAG 360

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 Db 2821 TTGTGTCTCCACTGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
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Oy	1893	GATTGGGAACAGAGAAATATCATTAATCTTTGATGAGCCCTGACAGAGATGAGCCCTCT	1952
Db	1799	GATTGGGAACAGAGAAATATCATTAATCTTTGATGAGCCCTGACAGAGATGAGCCCTCT	1858
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Oy	2193	GAATATACGACATTTGATGCTGACAGATATTCACATATATGACATATGACATATGAC	2252
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Db	2219	CATCATACAGAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2278
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Db	2519	ACCTAGTTACCTGATACACAGAACTCTTGTCTTTCAGAGATGATGATGATGATGATGAT	2578
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Db	2579	AGACCCATGCTTACAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2638
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Db	2759	GACTAAATATATTTGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT	2818
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Oy	3033	CGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3092
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Db	3059	AAATATATATATATATATTTACAGAGAGATTTTCTGAGAGATGATGATGATGATGAT	3118
Oy	3213	AATGACAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3272
Db	3119	AATGACAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3178
Oy	3273	CAGATATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3332
Db	3179	CAGATATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3238
Oy	3333	ATGCTATACAGATATATTTATATATATGATGATGATGATGATGATGATGATGATGAT	3392
Db	3239	ATGCTATACAGATATATTTATATATATGATGATGATGATGATGATGATGATGATGAT	3298
Oy	3393	TTTTTTTTGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3452
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Oy	3453	TGCTTGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	3509
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RESULT 6

HISCFR2UB 3248 bp DNA Linear PRT 25-JUN-1997

HISCFR2UB

H.sapiens fgfr2 gene (exon 5).

DEFINITION

Accession 266410.1 GI:120062

Keywords FGFR2 gene; fibroblast growth factor receptor 2.

Source Homo sapiens.

Organism Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Title New point mutations in FGFR2 associated with Crozon syndrome

Journal Unpublished

Remark (sites)

2 (bases 1 to 3248)

Steinberger D.

Direct Submision

Submitted (20-Feb-1996) Steinberger D., Institute for Human

Genetics, University of Mainz, Germany, 35392

Genetic/Qualifiers

1..3248

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/isolate="proband 97"

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/chromosome="10"

/sex="Female"

/tissue_type="Blood"

[illegible]

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Db 1921 AACATGTGATGAAATATGACAGACCTTGTGGACGTGCGAGAGATTCACAAATATGACAT 1980
Oy 2242 TACAAAMAGCACAGATGGGCGGCTTCACATGCAATGATGGCTCCAGAACCCCTGTT 2301
Db 1981 TACAAAMAGCACAGATGGGCGGCTTCACATGCAATGATGGCTCCAGAACCCCTGTT 2040
Oy 2302 GATGAGATATACACTGATCAGAGATGATGTGTGCTGGCGGCTTTAATGTGGAGAGAT 2361
Db 2041 GATGAGATATACACTGATCAGAGATGATGTGTGCTGGCGGCTTTAATGTGGAGAGAT 2100
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RESULT 7
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LOCUS HISGFR2UA
DEFINITION H. sapiens fgfr2 gene.
ACCESSION Z69641.1 GI:1200061
VERSION 269641.1
KEYWORDS H. sapiens fibroblast growth factor receptor 2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REPERNCE 1 (bases 1 to 3248)
AUTHORS Steinberger,D., Mulliken,J. and Mueller U.
JOURNAL J. Clin. Invest. 103:111-121 (1999)
REMARK Unpublished
REFERENCE 2 (bases 1 to 3248)
AUTHORS Steinberger,D.
JOURNAL Direct Submission
SUBMITTER (20-FEB-1995) Steinberger D., Institute for human
Genetics, Location/Dualfilets
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Matches 3246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Dh	121	GACCCACACCAATATCCAAATCTCTCAACCAAGATATACCTGGCTGGCCAGGGGAG	1860
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 Oy 2212 CTGCGCAGATATTCACATATTAACATTAACAAAGACCAATGAGGCGGCTGTCA 2271
 Db 2360 CTGCGCAGATATTCACATATTAACATTAACAAAGACCAATGAGGCGGCTGTCA 2419
 Oy 2272 GTCAATGTGATGTGTGACAGAGCCGTGTGTATGTGATGATACATCAAGATGATGATG 2331
 Db 2420 GTCAATGTGATGTGTGACAGAGCCGTGTGTATGTGATGATACATCAAGATGATGATG 2479
 Oy 2332 TGTGCTTCTGGGCTGTTAATGTGGCAATCTTCACTTTAGGGGCTGTGCGCTTACCAAGG 2391
 Db 2480 TGTGCTTCTGGGCTGTTAATGTGGCAATCTTCACTTTAGGGGCTGTGCGCTTACCAAGG 2539
 Oy 2392 ATTCCGTGAGAGAACTTTTAAGTGTCTGTAAGAGAGGACACATGATGATGAGAGG 2451
 Db 2540 ATTCCGTGAGAGAACTTTTAAGTGTCTGTAAGAGAGGAGACACATGATGATGAGAGG 2599
 Oy 2452 AACGTGACAAAGACGTGATACATGATATGATGATGATGATGATGATGATGATGATG 2511
 Db 2600 AACGTGACAAAGACGTGATACATGATATGATGATGATGATGATGATGATGATGATG 2659
 Oy 2512 AGACACGTTTCAAGAGTTGCTGATAGAGCTGTGATGATGATGATGATGATGATGATGAT 2571
 Db 2660 AGACACGTTTCAAGAGTTGCTGATAGAGCTGTGATGATGATGATGATGATGATGATGAT 2719

2572 GAGGAACTTGGAGCTGAGCAAGCTCTGTCAGCAAGTATTCACCTAGTTACCGCTGACACA 2631
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2730 GAGGAACTTGGAGCTGAGCAAGCTCTGTCAGCAAGTATTCACCTAGTTACCGCTGACACA 2779
2632 AAAAAATTTGTTTCTTCAGAGAGATTTCTGTTTTTCTTCAGAGACCCCAAGCTCTACGAA 2691
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2780 AAAAAATTTGTTTCTTCAGAGAGATTTCTGTTTTTCTTCAGAGACCCCAAGCTCTACGAA 2839
2692 GCATGCTCTCTCAGTATCTCAGCAATTAAGGCGCTTTAAACAAAGAAAGTACTGTCT 2751
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2840 CCAATGCTCTCTCAGTATCTCAGCAATTAAGGCGCTTTAAACAAAGAAAGTACTGTCT 2899
2752 GCGTGTCCCAAAAGAGACACCTGSSAAAGCTTACCTACCTAGACAGGAGACCTATGCC 2811
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RESULT 10
AX329662 3244 bp DNA linear PAT 09-JAN-2002
LOCUS AX329662
DEFINITION Sequence 171 from Patent WO0194629.
ACCESSION AX329662
VERSION AX329662.1 GI:18102640
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 Young, P. E.; Augustus, M.; Carter, K. C.; Ebner, R. R.; Endress, G.,
"Detection of human chorionic gonadotropin (hCG) gene polymorphisms by
PCR and gene determination and therapeutic screening using signature
gene sets.
JOURNAL Patent: WO 0194629-A 171 13-DEC-2001;
Pharmaceuticals (US)
FEATURES
source 1..3244 /db-xref="Homo sapiens"
1..3244 /db-xref="taxon.9606"
BASE COUNT 861 a 795 c 852 g 736 t
ORIGIN
Query Match 62.6%; Score 2670.4; DB 6; Length 3244;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 3029; Conservative 0; Mismatches 1; Indels 348; Gaps 1;
1 CCCAAGACACATCTTGTGCTTTGAGATGTGCTCCCAACACCGGGGCTGCTGCTGCT 60
|||||
215 CCCAAGACACATCTTGTGCTTTGAGATGTGCTCCCAACACCGGGGCTGCTGCTGCT 274
61 TCCATCCGACCCAGCGGGGCTGCGGACACAAACAGAGTCCCGAGAGAGCTTCCATTC 120
DB TCCATCCGACCCAGCGGGGCTGCGGACACAAACAGAGTCCCGAGAGAGCTTCCATTC 334
121 AAGTATGTCAGACAGACGAGGAGCCCTCGCTCTGTCAGGCCACCGCAGGCTGAAGCA 180
DB AAGTATGTCAGACAGACGAGGAGCCCTCGCTCTGTCAGGCCACCGCAGGCTGAAGCA 394
335 AAGTATGTCAGACAGACGAGGAGCCCTCGCTCTGTCAGGCCACCGCAGGCTGAAGCA 394
181 TTGCGCTGATGTCATCCCGTGAAGAGAGTGTGAGATGAGATTAAGTCTCACTGAGCA 240
DB TTGCGCTGATGTCATCCCGTGAAGAGAGTGTGAGATGAGATTAAGTCTCACTGAGCA 454

241 TATGAGAAAGAGACCGGGGATTTGATACGTAACATGTCTACGTGGGTCTTCTATCTGCG 300
DB TATGAGAAAGAGACCGGGGATTTGATACGTAACATGTCTACGTGGGTCTTCTATCTGCG 514
301 CTGGTGTGGGTACCATGGACACCTGTGCTCGTGGCGGGGCTGCTCATGATTTAGTTAG 360
DB CTGGTGTGGGTACCATGGACACCTGTGCTCGTGGCGGGGCTGCTCATGATTTAGTTAG 574
515 CTGGTGTGGGTACCATGGACACCTGTGCTCGTGGCGGGGCTGCTCATGATTTAGTTAG 574
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841 CGGTGCTGAAAGACGGGAGAGATTATGACGAGAGCATCGCATTTGGAGGCTTCAAGATGA 900
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1175 ACTGTGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1134
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DB ACCTGTGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1234
1175 ACTGTGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1234
1021 GAGGAGTGTGCTACCGCGGACCAACCTGATGAGACAGCGGAGCGGCGGCAATGTGCTGACAGT 1080
DB GAGGAGTGTGCTACCGCGGACCAACCTGATGAGACAGCGGAGCGGCGGCAATGTGCTGACAGT 1284
1225 GAGGAGTGTGCTACCGCGGACCAACCTGATGAGACAGCGGAGCGGCGGCAATGTGCTGACAGT 1284
1081 GTGCGAGAGAGAGTGAAGTTGTGTCTGACAAAGTTTAAGTGAATGTCGACAGCCCAATCAAG 1140
DB GTGCGAGAGAGAGTGAAGTTGTGTCTGACAAAGTTTAAGTGAATGTCGACAGCCCAATCAAG 1354
1295 GTGCGAGAGAGAGTGAAGTTGTGTCTGACAAAGTTTAAGTGAATGTCGACAGCCCAATCAAG 1354
1141 TGGATCAACACCTGTGAAAGAAAGAGCAATTAATGAGGGGCGAGAGGGGCTGCTTACCTG 1200
DB TGGATCAACACCTGTGAAAGAAAGAGCAATTAATGAGGGGCGAGAGGGGCTGCTTACCTG 1414
1355 TGGATCAACACCTGTGAAAGAAAGAGCAATTAATGAGGGGCGAGAGGGGCTGCTTACCTG 1414
1201 AAGGTGTCAAGAGCGCGCGGTGTTAAACACACAGGACAAAGAGTATGAGTTCCTATATTT 1260
DB AAGGTGTCAAGAGCGCGCGGTGTTAAACACACAGGACAAAGAGTATGAGTTCCTATATTT 1426
1415 AAGGTGTCAAG----- 1426
1261 GCGATGTAACTTTTGAAGACGCTGGGGAAATATACGTGCTTGGCGGGTAAATCAATGGG 1320
DB GCGATGTAACTTTTGAAGACGCTGGGGAAATATACGTGCTTGGCGGGTAAATCAATGGG 1426
1427 ----- 1426

[illegible]


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Oy 1441 TGTATGTGTGTAACAGTATCTCTGTGCGAATGAGAACGACAGAACAGACCAAGATTCT 1500
Db 1427 ----- 1426
Oy 1501 AGACGACGACGGGTGTGCACAACTGACCAAAAGCTATCCCCCTGCGGAGACAGGTACAA 1560
Db 1427 ----- 1426
Oy 1561 GTTTCGGGTGATGATCAGCTCTCCATGAATCCACACACCCGCTGGTGAAGATACAA 1620
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Db 1607 GGTTCCTTTGGGACAGATGTGATCGTGGGACAGAGTGGATATTCACAAAGACCCCAAA 1800
Oy 1801 GAGGCGGTGACCGCTGGCGCTGACAAATGTTTCAAAAGATGATCCACAGAGAAAGACCTTCT 1860
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Db 1787 CTTTCTGGAGCTGACACAGATGAGGTGCGTATATGTGTATACGTATGACTCTTAA 1980
Oy 1981 GGCACCTCCGAGAAATACCTCGAGGCCGAGGACCCGGGATGAGATGATCCCTATAC 2040
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Db 1907 ATTAAACGCTGTTCTGAGAGAGACAGATGACACTTCAAGGATTTGGTGTATGACAGCTACAG 2100
Oy 2101 CTTGCGCAGAGCATGTGAGATACCTTGCTCCAAAATGATATTCATCAATTTAGACACC 2160
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Db 2507 TGTCTTCAGAGATATGATCTGTGTGTGTCTGACAGACCCGATGCTGTACAGCAATCCCTT 2700
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Oy 2761 CAAGAGACACGACATGCGGACACAGACAGATGATGACAGAGAGACATGCTCTCCAGAC 2820
Db 2627 CAAGAGACACGACATGCGGACACAGACAGATGATGACAGAGAGACATGCTCTCCAGAC 2820
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Oy 3121 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
Db 2987 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
Oy 3181 TATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3240
Db 3047 TATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3240
Oy 3241 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
Db 3107 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3300
Oy 3301 GAGGTGAGAAATACCTTGTCTTGCGGAAATGATGATGATGATGATGATGATGATGATGATG 3360
Db 3167 GAGGTGAGAAATACCTTGTCTTGCGGAAATGATGATGATGATGATGATGATGATGATGATG 3360
Oy 3361 TGTGATATATACAAACAA 3378
Db 3227 TGTGATATATACAAACAA 3344

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RESULT 12
AF211257 3809 bp mRNA linear MAN 05-JAN-2000
DEFINITION Canis familiaris fibroblast growth factor receptor 2 (FGFR2) mRNA.
ACCESSION AF211257.1 GI:6671356
VERSION AF211257.1
KEYWORDS Canis familiaris.
SOURCE Eukaryota: Chordata: Cranialia: Vertebrata: Euteleostomi:
Organism: Euteleostei: Carnivora: Flsiipedidae: Canidae: Canis.
REFERENCE 1 (bases 1 to 3809)

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Db 1753 GAGATATCAACATATATAGACTATATACAAAAGACCAATATGGCGAGCTTCGCGTCAAGT 1812
Oy 2279 GGAATGGCTCCAGAGACCCGTTTGAGAGAGATATACCTCATTCAGATGATGCTGGTCT 2338
Db 1813 GGAATGGCTCCAGAGACCCGTTTGATGATGAGGTACCCATCAGATGATGATGATGCT 1872
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Oy 2399 TGGGGAACCTTTTATATGCTGTGAAGGAAGAGACAAATGATGATGATGATGATGATGATG 2458
Db 1933 TGGGGAACCTTTTATATGAGCTGTCAAGAGAGGGGACAGAGATGAGACAGAGAAATGCA 1992
Oy 2459 CCAGCAACTGATACATGATATGATGAGAGATCTTGGCAGTCAGTACGCTCCAGAGACCA 2518
Db 1993 CCAGCAACTGATATGATGATATGAGAGATCTTGGCAGTCAGTACGCTCCAGAGACCA 2052
Oy 2519 GCTTCCAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2578
Db 2053 GCTTCCAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2112
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Db 2113 ACTTGGACCTTCAGCAACCTCTGAGACAGATATTCACCTGATTTACCTGTACACAGAGAT 2172
Oy 2639 CTGTGTTCTTCAGAGAGATGATGCTGTTTTTCTTCAGACCCGACGATCTTACAGACATG 2698
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Db 2353 GCGGGGTGCGCTGCTGTATATGATGATGATGATGATGATGATGATGATGATGATGATG 2411
Oy 2879 CATATGTTAAG-ATTATACAGCTGAAACCTGTATATCTGCCAGAGAGAGAGAG 2937
Db 2412 CACAGGTTAAGAGATTTATAGGTTGAGAGAGATGATATATCTTACAGAGAGAGAGAT 2471
Oy 2938 GTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2997
Db 2472 GTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2528
Oy 2998 CTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3056
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Oy 3057 GTATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3116
Db 2589 GTATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2648
Oy 3117 GTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3175
Db 2649 GTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2708
Oy 3176 GAGAGTATTTTGTATGATTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3225
Db 2709 GAGAGTATTTTGTATGATTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2768
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Oy 3348 TTTATATATATATGATATATATATATATATATATATATATATATATATATATATATAT 3396
Db 2889 TTTATATATATATGATATATATATATATATATATATATATATATATATATATATATAT 2948
Oy 3397 -...TTTTTATATATATATATATATATATATATATATATATATATATATATATAT 3454
Db 2949 TATTTGTATATATATATATATATATATATATATATATATATATATATATATATATAT 3008
Oy 3455 CTGAGCACTTACTAGTATATATATATATATATATATATATATATATATATATATATATAT 3513
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Db 3069 TTTGGGGAATATATATATATATATATATATATATATATATATATATATATATATATAT 3126
Oy 3573 CTATACACTCTTAAATATGCCCCCTTTAAATGAAGACATATATATATATATATATATATAT 3632
Db 3127 CTATACACTCTTAAATATGCCCCCTTAAATGAAGACATATATATATATATATATATATAT 3185
Oy 3633 GGTGTCACACCTGTGATATATATATATATATATATATATATATATATATATATATATAT 3692
Db 3186 GGTGTCACACCTGTGATATATATATATATATATATATATATATATATATATATATATAT 3245
Oy 3693 TACAGAGCTCTCTT-...AAAGATATATATATATATATATATATATATATATATATATATAT 3751
Db 3246 TACAGAGCTCTCTT-...AAAGATATATATATATATATATATATATATATATATATATATAT 3305
Oy 3752 ATGATACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3811
Db 3306 ATGATACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3364
Oy 3812 TCGATATATATCTG-ATTTCTTCAGTATATATATATATATATATATATATATATATATATAT 3869
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Oy 3929 TGTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3989
Db 3484 TGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3543
Oy 3989 AGAGACTACCAAAAGATCCACCTGATATATATATATATATATATATATATATATATAT 4047
Db 3544 AGAGACTACCAAAAGATCCACCTGATATATATATATATATATATATATATATATATATAT 3603
Oy 4048 GCTCTGTGAT-CTAAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4106
Db 3604 GCTCTGTGAT-CTAAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3663
Oy 4107 GTGCAAGATGAATGAGATATATATATATATATATATATATATATATATATATATATAT 4166
Db 3664 ATTAACACTGATATATATATATATATATATATATATATATATATATATATATATATAT 3723
Oy 4167 ATTAACACTGATATATATATATATATATATATATATATATATATATATATATATATAT 4226
Db 3724 ATTAACACTGATATATATATATATATATATATATATATATATATATATATATATATAT 3783
Oy 4227 AAGACAAATATATATATATATATATATATATATATATATATATATATATATATAT 4282
Db 3784 AAGACAAATATATATATATATATATATATATATATATATATATATATATATATATAT 3809

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RESULT 13
 HUNGERFZA 3080 bp mRNA P1: 08-NOV-1994
 LOCUS 3080 bp
 DEFINITION Homo sapiens fibroblast growth factor receptor 2 (lrb) (PFR2) mRNA,
 accession M97193
 version M97193.1 GI:182566

Db	421	GAAGATTTTGTGACGTGGAGAACATGAAACACAAACACACCATACCTGGACCAACAGAA	480
Qy	754	AAGATGGAAAGAGGGTGCATGTGTGTGCTGTGGCCACACCTCTCAACTCTTCCTGCCA	813
Db	481	AAGATGTGGAAAGAGGGTGCATGTGTGTGCTGTGGCCACACCTCTCAACTCTTCCTGCCA	540
Qy	814	CCCGGGGGGAGCCCATATCCCAACCTCCGCGTGGCTGAAAGAGAGATTTAACAG	873
Db	541	GGCGGGGGGAGCCCATATCCCAACCTCCGCGTGGCTGAAAGAGAGATTTAACAG	933
Qy	874	GAGCATGTGATTTGAGAGGCTACAAAGTACGAACACGACATGGACCTCATATGGACAA	930
Db	601	GAGCATGTGATTTGAGAGGCTACAAAGTACGAACACGACATGGACCTCATATGGACAA	660
Qy	934	GTGGTGTGCTCTGTACAAAGGAAATTAATACCTGTGTGTGTGGAGAAAGTAATGGGTGCAT	934
Db	661	GTGGTGTGCTCTGTACAAAGGAAATTAATACCTGTGTGTGTGGAGAAAGTAATGGGTGCAT	720
Qy	994	AATCCAGCTACACACTGATGTGTTGTGGAGCATGGCTCTACCGACATCTCCACAC	105
Db	721	AATCCAGCTACACACTGATGTGTTGTGGAGCATGGCTCTACCGACATCTCCACAC	780
Qy	1054	GACATGTGGGAAATATGCTCTCCATGATGTGGAGAGACATGAAGTTTCTCCAAAGTT	1111
Db	781	GACATGTGGGAAATATGCTCTCCATGATGTGGAGAGACATGAAGTTTCTCCAAAGTT	847
Qy	1114	TACATGATGATGCGAACGCGCAGACATCTCATGTGACACGATGGAAAGAGAGGCGACTAA	1140
Db	841	TACATGATGATGCGAACGCGCAGACATCTCATGTGACACGATGGAAAGAGAGGCGACTAA	900
Qy	1174	TAGGAGGATGCGAACGCGCTGCCCTACCTCAAGATGTCTACAGGCGCGCGGTGTAAACAC	123
Db	901	TAGGAGGCGCGAAGGCGCGCTGCCCTACCTCAAGATGTCTACAGGCGCGCGGTGTAAACAC	960
Qy	1234	GACAAACAGATTAGCTTCTCTAATTTGGAATGTAACTTTGAGACACTGTGGCAAT	123
Db	961	GACAAACAGATTAGCTTCTCTAATTTGGAATGTAACTTTGAGACACTGTGGCAAT	102
Qy	1294	ACGCTCTGTGGGGGATTAATCTAATTTGGGAATATCTTCACTGATGATGGTGTGACAGTTG	13
Db	1021	ACGCTCTGTGGGGGATTAATCTAATTTGGGAATATCTTCACTGATGATGGTGTGACAGTTG	100
Qy	1354	CCAGCGCTGTGAGAGAGAAAGAGATTAACGTTCCCAATCACTGAGATTAAGTAACTT	14
Db	1081	CCAGCGCTGTGAGAGAGAAAGAGATTAACGTTCCCAATCACTGAGATTAAGTAACTT	114
Qy	1414	TATCTCATATAGGGGTCTTAAATGCTCGATATGGTGTGAACAGTCACTGTGTGGCAATG	120
Db	1141	TATCTCATATAGGGGTCTTAAATGCTCGATATGGTGTGAACAGTCACTGTGTGGCAATG	120
Qy	1474	AAGAACATGACAAAGACGACACACTTACGACGACGACGCGCTGTCCAAAGCTTCAAA	15
Db	1201	AAGAACATGACAAAGACGACACACTTACGACGACGACGCGCTGTCCAAAGCTTCAAA	120
Qy	1534	CGTATATCCCTGTGGAGAGACAGTAAACAAATTTGGGTATGATCACTCTCAATCACTG	135
Db	1261	CGTATATCCCTGTGGAGAGAGTAAACAAATTTGGGTATGATCACTCTCAATCACTG	135
Qy	1594	AACACCCGCTGTGATGATTAACACAGCTCTCTTCAACGCGAAGACCCCATCTGTG	16
Db	1321	AACACCCGCTGTGATGATTAACACAGCTCTCTTCAACGCGAAGACCCCATCTGTG	130
Qy	1654	GCAGAGGATGTGATGATTAACACAGCTCTCTTCAACGCGAAGACCCCATCTGTG	17
Db	1381	GCAGAGGATGTGATGATTAACACAGCTCTCTTCAACGCGAAGACCCCATCTGTG	14
Qy	1714	GTGACATGTGGCAAGCCTGTGGAGAAAGTGTCTTTGGGAGAGTGTCTATGTGCGAGACA	17
Db	1441	GTGACATGTGGCAAGCCTGTGGAGAAAGTGTCTTTGGGAGAGTGTCTATGTGCGAGACA	15
Qy	1774	GTGAGGATTTGCAAGAGACACCCCAAGACGAGCGGTGACGCTGCGTCAAGATCTGTAA	18

[illegible]

Job time : 7248 secs

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Db 1435 TGGGAGCTTTCGAAAGATTAAGCTGACACCTGGGCAACCCCTGGGAGAGCTTCCTTGCG 1494
Oy 1753 CAAGTGGTCATGCGGGAACCAAGTGGGAATTGACAAAGACAAAGCCAGAGAGGCGGTCAAC 1812
Db 1495 CAAGTGGTCATGCGGGAACCAAGTGGGAATTGACAAAGACAAAGCCAGAGAGGCGGTCAAC 1554
Oy 1813 GTGGCGGTGAAGATGTTGAAGAGATGGCAGACAGAAAGACCTTCTGTATCTGGTGCA 1872
Db 1555 GTGGCGGTGAAGATGTTGAAGAGATGGCAGACAGAAAGACCTTCTGTATCTGGTGCA 1614
Oy 1873 GAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1932
Db 1615 GAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1674
Oy 1933 TGGCAGACAGATGAGGCTCTCATATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1992
Db 1675 TGCACACAGATGAGGCTCTCATATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1734
Oy 1993 GAATACCTCCAGCCCGAGCCAGCCCGGATGAGATGATGATGATGATGATGATGATGATGATG 2052
Db 1735 GAATACCTCCAGCCCGAGCCAGCCCGGATGAGATGATGATGATGATGATGATGATGATGATG 1794
Oy 2053 CCTGAGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2112
Db 1795 CCTGAGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1854
Oy 2113 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2172
Db 1855 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1914
Oy 2173 GTTACAGAGAAACAATGTGATGAAATATGACAGCTTGGACTGGCAGAGATATCAACAT 2232
Db 1915 GTTACAGAGAAACAATGTGATGAAATATGACAGCTTGGACTGGCAGAGATATCAACAT 1974
Oy 2233 ATAGACTATTACAAAGAACACCAATGCGCGCTTCCAGTCAATGATGATGATGATGATGATG 2292
Db 1975 ATAGACTATTACAAAGAACACCAATGCGCGCTTCCAGTCAATGATGATGATGATGATGATG 2034
Oy 2293 GCCCTGTTGATAGATATGACACTCATGATGATGATGATGATGATGATGATGATGATGATG 2352
Db 2035 GCCCTGTTGATAGATATGACACTCATGATGATGATGATGATGATGATGATGATGATGATG 2094
Oy 2353 TGGGAGATCTTCACTTAAAGGCGGTCGCGTACGAGAGATGCGGTGAGAACTTTT 2412
Db 2095 TGGGAGATCTTCACTTAAAGGCGGTCGCGTACGAGAGATGCGGTGAGAACTTTT 2154
Oy 2413 AAGCTGCTGAGAGAGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2472
Db 2155 AAGCTGCTGAGAGAGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2214
Oy 2473 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2532
Db 2215 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2274
Oy 2533 GTAGAAAGACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2592
Db 2275 GTAGAAAGACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2334
Oy 2593 CAAGCTGCTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2652
Db 2335 CAAGCTGCTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2394
Oy 2653 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2712
Db 2395 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2454
Oy 2713 CACATTAAGCGCATGTGTTAAACATGA 2739
Db 2455 CACATTAAGCGCATGTGTTAAACATGA 2481

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1141 TGGATCAGCAGCTGAGAAAGAGAGGCAAGTAATACGGGGCCGAGCGGCTGACCTC 1200
 Db 1141 TGGATCAGCAGCTGAGAAAGAGAGGCAAGTAATACGGGGCCGAGCGGCTGACCTC 1200
 Oy 1201 AAGGCTTCAGAGCGCGCGGGTGTAAACACAGCGGCAAGAGATGAGAGTCTGTATTT 1260
 Db 1201 AAGGCTTCAGAGCGCGCGGGTGTAAACACAGCGGCAAGAGATGAGAGTCTGTATTT 1260
 Oy 1261 CGGAAATACCTTTTGAAGACGCTGGGGAAATATACGTGCTTGGCGGGTAACTTATGGG 1320
 Db 1261 CGGAAATACCTTTTGAAGACGCTGGGGAAATATACGTGCTTGGCGGGTAACTTATGGG 1320
 Oy 1321 ATATCTCTTCACCTGCACTGGTGAAGATCTGCGAGCGGCTCGAAGAAAGAGAGATT 1380
 Db 1321 ATATCTCTTCACCTGCACTGGTGAAGATCTGCGAGCGGCTCGAAGAAAGAGAGATT 1380
 Oy 1381 ACGAGCTCCCGAGAGTACCTGGAGATACCCATTATGTGCATAGGGGCTCTTCTTAATGCC 1440
 Db 1381 ACGAGCTCCCGAGAGTACCTGGAGATACCCATTATGTGCATAGGGGCTCTTCTTAATGCC 1440
 Oy 1441 TGTATGAGTGTAAACAGTCAATCCCTGTGCCGAGTAAGAAAGACAGCAAGAACGAGCTTC 1500
 Db 1441 TGTATGAGTGTAAACAGTCAATCCCTGTGCCGAGTAAGAAAGACAGCAAGAACGAGCTTC 1500
 Oy 1501 AAGAGCTACCGGGGTGTGCAAGCTGCAACAGCTGCAATCCCTGTGCCGAGTAAGAA 1560
 Db 1501 AAGAGCTACCGGGGTGTGCAAGCTGCAACAGCTGCAATCCCTGTGCCGAGTAAGAA 1560
 Oy 1561 GTTTGGGCTGAGTCCAGCTCTCCATGATCAATCAACACCCGGGTGGTAGAGTAACAACA 1620
 Db 1561 GTTTGGGCTGAGTCCAGCTCTCCATGATCAATCAACACCCGGGTGGTAGAGTAACAACA 1620
 Oy 1621 CGGCTCTCTTCAACGGGCAACACCCGCAAGTGGTGGCAAGGGTCTCGAGATGAACCTTCA 1680
 Db 1621 CGGCTCTCTTCAACGGGCAACACCCGCAAGTGGTGGCAAGGGTCTCGAGATGAACCTTCA 1680
 Oy 1681 GAGACACCAAAATGSGAAGTTTCCAAAGATATAGCTGACACTGGGCAAGGCCCTGGGAGAA 1740
 Db 1681 GAGACACCAAAATGSGAAGTTTCCAAAGATATAGCTGACACTGGGCAAGGCCCTGGGAGAA 1740
 Oy 1741 GGTGGCTTGGGCGCAAGTGTCAATGGCGGAAGAGATGGGAATGACAAAGACCCCTGGAGAA 1800
 Db 1741 GGTGGCTTGGGCGCAAGTGTCAATGGCGGAAGAGATGGGAATGACAAAGACCCCTGGAGAA 1800
 Oy 1801 GAGGCGGTTCACCGTGGCCCTGAGATGTGTAAAGATATGTCACAGGAAAGACCTTTCT 1860
 Db 1801 GAGGCGGTTCACCGTGGCCCTGAGATGTGTAAAGATATGTCACAGGAAAGACCTTTCT 1860
 Oy 1861 GATCTGCTGTGTAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 Db 1861 GATCTGCTGTGTAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 Oy 1921 GTTGTGGAGCTGTGACACAGATGAGGCTGTCTATGTCTCATAGTTCATAGTATGATGATGAT 1980
 Db 1921 GTTGTGGAGCTGTGACACAGATGAGGCTGTCTATGTCTCATAGTTCATAGTATGATGATGAT 1980
 Oy 1981 GGCAGACCTCCAGAAATACCTCCAGACCCGAGAGGCCACCCGAGAGAGAGTACCTCATGAC 2040
 Db 1981 GGCAGACCTCCAGAAATACCTCCAGACCCGAGAGGCCACCCGAGAGAGAGTACCTCATGAC 2040
 Oy 2041 ATTAAACCGTGTCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 Db 2041 ATTAAACCGTGTCTGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2100
 Oy 2101 CTGGGCAAGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Db 2101 CTGGGCAAGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Oy 2161 AAGAAATGTTTGGTAAAGAAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
 Db 2161 AAGAAATGTTTGGTAAAGAAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2220

2221 GATATCAACATTAAGACTATTACAAAAAAGACCAATGCGCGGCTTCCAGTCAAGTGG 2280
 Db 2221 GATATCAACATTAAGACTATTACAAAAAAGACCAATGCGCGGCTTCCAGTCAAGTGG 2280
 Oy 2281 ATGGCTCCAGAGACCCGTGTGATAGTAACTATACACTATACAGAGATGATGATGATGATGAT 2340
 Db 2281 ATGGCTCCAGAGACCCGTGTGATAGTAACTATACACTATACAGAGATGATGATGATGATGAT 2340
 Oy 2341 GGGGGTAAATGAGAGATCTCAATTTTGGGGGGCGGCGCTACCCAGAGATGATGATGATGAT 2400
 Db 2341 GGGGGTAAATGAGAGATCTCAATTTTGGGGGGCGGCGCTACCCAGAGATGATGATGATGAT 2400
 Oy 2401 GAGAGACTTTTAAGCTGCTGAGAGAGAGACAGAGATGATTAACCCAGCAATGCGAGACC 2460
 Db 2401 GAGAGACTTTTAAGCTGCTGAGAGAGAGACAGAGATGATTAACCCAGCAATGCGAGACC 2460
 Oy 2461 AAGCAAGTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
 Db 2461 AAGCAAGTACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
 Oy 2521 TTCAACGACTTGGTAAAGAAATGAGATGATGATGATGATGATGATGATGATGATGATGAT 2580
 Db 2521 TTCAACGACTTGGTAAAGAAATGAGATGATGATGATGATGATGATGATGATGATGATGAT 2580
 Oy 2581 TTGAGCTCAGACCACTCTGAACAGATATACCTAGTACCTGCAACAAAGATTTCT 2640
 Db 2581 TTGAGCTCAGACCACTCTGAACAGATATACCTAGTACCTGCAACAAAGATTTCT 2640
 Oy 2641 TGTGCTTCAGAGATTAATGCTGTTTTTCTTCAGAGCCCATGCTTACGAACAGCTTT 2700
 Db 2641 TGTGCTTCAGAGATTAATGCTGTTTTTCTTCAGAGCCCATGCTTACGAACAGCTTT 2700
 Oy 2701 CCTGATATCCACATTAAGCGGAGGTGTTAAACATGAATGATGATGATGATGATGATGAT 2760
 Db 2701 CCTGATATCCACATTAAGCGGAGGTGTTAAACATGAATGATGATGATGATGATGATGAT 2760
 Oy 2761 CAAGACAGACAGTATGGAACCTAGCTACCTGACCTGACCTGACCTGACCTGACCT 2820
 Db 2761 CAAGACAGACAGTATGGAACCTAGCTACCTGACCTGACCTGACCTGACCTGACCT 2820
 Oy 2821 TTGTTGTCTCACTGTATATATGATATAGATAGAGAGTAAATATGGAAGAAATATGATGAT 2880
 Db 2821 TTGTTGTCTCACTGTATATATGATATAGATAGAGAGTAAATATGGAAGAAATATGATGAT 2880
 Oy 2881 TATGTGTAAAGATTATACATTTGAAACCTGTATATCTGCTCCAGAGAGAGAGAGCTT 2940
 Db 2881 TATGTGTAAAGATTATACATTTGAAACCTGTATATCTGCTCCAGAGAGAGAGAGCTT 2940
 Oy 2941 TCTGGACAGATGATCTGCACAGACCACTATGTAACGCTCTCTACGCGCTGCTGCTG 3000
 Db 2941 TCTGGACAGATGATCTGCACAGACCACTATGTAACGCTCTCTACGCGCTGCTGCTG 3000
 Oy 3001 GCGTGTGACAGCTAGAGACTCAAGGTGAGAGCTGCGTGTGCTCTCTGTTAAATTTTGTA 3060
 Db 3001 GCGTGTGACAGCTAGAGACTCAAGGTGAGAGCTGCGTGTGCTCTCTGTTAAATTTTGTA 3060
 Oy 3061 TAATGAGAGAGATTATGTGACACACACTTACAGAGACCAATAGATATATAGTGC 3120
 Db 3061 TAATGAGAGAGATTATGTGACACACACTTACAGAGACCAATAGATATATAGTGC 3120
 Oy 3121 TGCATGATATGTAATATATTAATTTATGTAATATATATATATATATATATATATATATAT 3180
 Db 3121 TGCATGATATGTAATATATTAATTTATGTAATATATATATATATATATATATATATATAT 3180
 Oy 3181 TATTTTGTGATGATTAATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
 Db 3181 TATTTTGTGATGATTAATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
 Oy 3241 TTTTAAATAGCTATTTGCTAAATCGTGTCTTACAGATATATTTCTTAAATTTGTCAGAGAA 3300
 Db 3241 TTTTAAATAGCTATTTGCTAAATCGTGTCTTACAGATATATTTCTTAAATTTGTCAGAGAA 3300
 Oy 3301 GAGGTGAGAAAAATCTTTGCTTCAAGAGAAATGATATGATGATTAATTAATTAAT 3360

XX The present invention describes a method (M1) for screening for an
 CC anti-cancer agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-cancer activity, and determining a change in
 CC expression of at least one gene (1) of a single nucleotide polymorphism
 CC comprising a sequence (5') selected from 8447 sequences (given in A616164
 CC to A6170110), or is at least 95% identical to (5'), where a change in
 CC expression is indicative of anti-neoplastic activity. (1) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC agents that have anti-cancer activity and can be used for producing a product which
 CC is the data collected with the method. The anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to produce an anti-neoplastic agent as a
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer, such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC metastatic lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.

XX Sequence 4268 BP: 1199 A: 964 C: 1028 G: 1077 T: 0 other:

Query Match 100.0%; Score 4268; Mch 24; Length 4268;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 4268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 CCCAAGGACACCTCTTCTGCTGGTTCAGTCCGACCAACCGGCGCTCTGCTGCTTC 60
 Db 1 CCCAAGGACACCTCTTCTGCTGGTTCAGTCCGACCAACCGGCGCTCTGCTGCTTC 60
 0Y 61 TCCATCCGACCCACCGCGGGCGCGGCGACACACAGAGTCCGAGAGAGGCTTCATTC 120
 Db 61 TCCATCCGACCCACCGCGGGCGCGGCGACACACAGAGTCCGAGAGAGGCTTCATTC 120
 0Y 121 AAGTACGTCAGACAGCAGCGACGCGCTGCTGCTGACGCGCCAGCGAGCTGAAGCA 180
 Db 121 AAGTACGTCAGACAGCAGCGACGCGCTGCTGCTGACGCGCCAGCGAGCTGAAGCA 180
 0Y 121 AAGTACGTCAGACAGCAGCGACGCGCTGCTGCTGACGCGCCAGCGAGCTTCATTC 120
 Db 121 AAGTACGTCAGACAGCAGCGACGCGCTGCTGCTGACGCGCCAGCGAGCTTCATTC 120
 0Y 181 TTTCCGCTGAGTCCATCCCTGATGAGAGAGTGTGCAGATGGATTATGCTGCATGGGA 240
 Db 181 TTTCCGCTGAGTCCATCCCTGATGAGAGAGTGTGCAGATGGATTATGCTGCATGGGA 240
 0Y 241 TATGAGAGAGACCGGGATTGTACCGGTACCGATGACGTGGGTGCTTCATGTCGC 300
 Db 241 TATGAGAGAGACCGGGATTGTACCGGTACCGATGACGTGGGTGCTTCATGTCGC 300
 0Y 301 CTGGCTGCTGTCACATGAGCAACCTGTCTGCGCCGCGGCTCTCTTACGTTAGTTGA 360
 Db 301 CTGGCTGCTGTCACATGAGCAACCTGTCTGCGCCGCGGCTCTCTTACGTTAGTTGA 360
 0Y 361 GATACACATTAAGACAGAGACGACCAACAAATACCAAAATCTGCACAGCAATG 420
 Db 361 GATACACATTAAGACAGAGACGACCAACAAATACCAAAATCTGCACAGCAATG 420
 0Y 421 TACGTGCTGCGCAGGACGCTTACAGATGAGTGGCTGTGCTTGAAGATGCCGCTG 480
 Db 421 TACGTGCTGCGCAGGACGCTTACAGATGAGTGGCTGTGCTTGAAGATGCCGCTG 480
 0Y 481 ATCACTGATTAAGATGAGATGGGTGCTACTTGGGCGCCACAAATAGACAGCTTATGG 540
 Db 481 ATCACTGATTAAGATGAGATGGGTGCTACTTGGGCGCCACAAATAGACAGCTTATGG 540
 0Y 541 GAGTCTGCGATTAAGAGGCGCCACAGCCCAACAACTCTGCGCTCTATGCTTGTATGCC 600
 Db 541 GAGTCTGCGATTAAGAGGCGCCACAGCCCAACAACTCTGCGCTCTATGCTTGTATGCC 600
 0Y 601 ACTAGGACTGTAGACAGTGAACCTGTGATTCATGATGATATGCTACAGATGCCATTC 660
 Db 601 ACTAGGACTGTAGACAGTGAACCTGTGATTCATGATGATATGCTACAGATGCCATTC 660
 0Y 661 TCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 Db 661 TCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 0Y 720 TCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 Db 720 TCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720

0Y 721 AACAGAGAGACACCATCTAGTACACACACACACACACACACACACACACACACAC 780
 Db 721 AACAGAGAGACACCATCTAGTACACACACACACACACACACACACACACACACAC 780
 0Y 781 CTGCGCGCCACACATCTCAAGTTTCTGCTGCGCCAGCGCGGGGGAGACCAATGCGCAACATG 840
 Db 781 CTGCGCGCCACACATCTCAAGTTTCTGCTGCGCCAGCGCGGGGGAGACCAATGCGCAACATG 840
 0Y 841 CGGTGGGTGAGAGAGAGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 841 CGGTGGGTGAGAGAGAGATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 0Y 901 GCAACACACACAGTACAGCTTATGAGAAAGTGTGTCCATCTGACAAAGGAAATAT 960
 Db 901 GCAACACACACAGTACAGCTTATGAGAAAGTGTGTCCATCTGACAAAGGAAATAT 960
 0Y 961 ACCTGTGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Db 961 ACCTGTGTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 0Y 1021 GACCATACCTCTACAGCGCCCATCTCTCCACAGCGGACCTGCGGCAATGCTCCACATG 1080
 Db 1021 GACCATACCTCTACAGCGCCCATCTCTCCACAGCGGACCTGCGGCAATGCTCCACATG 1080
 0Y 1081 GTGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 Db 1081 GTGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 0Y 1141 TGGATCTAGACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 Db 1141 TGGATCTAGACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 0Y 1201 AAGGTTCTCAAGAGCGCGCGGTGTAAACACACAGCAAGAAAGATGAGGTTCTGATAT 1260
 Db 1201 AAGGTTCTCAAGAGCGCGCGGTGTAAACACACAGCAAGAAAGATGAGGTTCTGATAT 1260
 0Y 1261 AAGGTTCTCAAGAGCGCGCGGTGTAAACACACAGCAAGAAAGATGAGGTTCTGATAT 1320
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 Db 1321 ATATCTTCTCACTGTGACATGTTGATGACAGTGTGTGACAGCGCTGAGAAAGAAAGAGAT 1380
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 0Y 1441 TGTATGAGTGTAGACAGTATCTGTGCGAGTGAAGAAAGACAGCAAGAGACAGAT 1500
 Db 1441 TGTATGAGTGTAGACAGTATCTGTGCGAGTGAAGAAAGACAGCAAGAGACAGAT 1500
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 Db 1501 ACAGGTTCTCAAGAGCGCGCGGTGTAAACACACAGCAAGAAAGATGAGGTTCTGATAT 1560
 0Y 1561 GTTTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 Db 1561 GTTTCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 0Y 1621 GCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 Db 1621 GCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
 0Y 1681 GAGGAGCCCAAAATGAGGATTTTCAAAAGATATGATGATGATGATGATGATGATGAT 1740
 Db 1681 GAGGAGCCCAAAATGAGGATTTTCAAAAGATATGATGATGATGATGATGATGATGAT 1740
 0Y 1741 GCTTGTCTGTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 Db 1741 GCTTGTCTGTGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
 0Y 1801 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
 Db 1801 GAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860

[illegible][illegible]

Oy 2521 TTCAAGCACTGGTGCAGAGCTGGATGCATATTCACCTCCACACCAATGAGAGATAC 2580
 Db 2521 TTCAAGCACTGGTGCAGAGCTGGATGCATATTCACCTCCACACCAATGAGAGATAC 2580
 Oy 2581 TTGGACCTCAGCCACCTCCGACACAGATATTCACCTGGTACCTGGACACAGAAATGCTC 2640
 Db 2581 TTGGACCTCAGCCACCTCCGACACAGATATTCACCTGGTACCTGGACACAGAAATGCTC 2640
 Oy 2641 TGTGTTCAAGAGATGATGATGTTTTTTCTCCAGACCCCATGCTTACAGACACCTGCTT 2700
 Db 2641 TGTGTTCAAGAGATGATGATGTTTTTTCTCCAGACCCCATGCTTACAGACACCTGCTT 2700
 Oy 2701 CCTCAGATTCAGACATTAAGAGCATTTTAAACATGATGATGCTGCTGCTGCTGCTGCT 2760
 Db 2701 CCTCAGATTCAGACATTAAGAGCATTTTAAACATGATGATGCTGCTGCTGCTGCTGCT 2760
 Oy 2761 CAACAGACACCTGAGACACCTGACCTACCTACCTAGACAGACACCTGCTGCTGCTGCT 2820
 Db 2761 CAACAGACACCTGAGACACCTGACCTACCTACCTAGACAGACACCTGCTGCTGCTGCT 2820
 Oy 2821 TTTGTTGCTCAGCTGTATATATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
 Db 2821 TTTGTTGCTCAGCTGTATATATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
 Oy 2881 TATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
 Db 2881 TATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940
 Oy 2941 TCTGAGACAGTGCACCTCCACACACCTGATACCTGCTACCTGCTGCTGCTGCTGCT 3000
 Db 2941 TCTGAGACAGTGCACCTCCACACACCTGATACCTGCTACCTGCTGCTGCTGCTGCT 3000
 Oy 3001 GCTGAGACAGTGCACCTCCACACACCTGATACCTGCTGCTGCTGCTGCTGCTGCT 3060
 Db 3001 GCTGAGACAGTGCACCTCCACACACCTGATACCTGCTGCTGCTGCTGCTGCTGCT 3060
 Oy 3061 TAATGAGAGATTTATGTCAGACACCTGATACAGACACCAATGACATATATAGGTGC 3120
 Db 3061 TAATGAGAGATTTATGTCAGACACCTGATACAGACACCAATGACATATATAGGTGC 3120
 Oy 3121 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
 Db 3121 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
 Oy 3181 TATTTTGTGATGATGATTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
 Db 3181 TATTTTGTGATGATGATTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 3240
 Oy 3241 TTTTAAATGATTTGCTAAATGCTGCTTCCACAAATTTCTTAAATTTTCCACGAGCA 3300
 Db 3241 TTTTAAATGATTTGCTAAATGCTGCTTCCACAAATTTCTTAAATTTTCCACGAGCA 3300
 Oy 3301 GAGTGCAGAAAATACCTTGGCTTCCAGGAAAATGCTATTAATTTAATTAAT 3360
 Db 3301 GAGTGCAGAAAATACCTTGGCTTCCAGGAAAATGCTATTAATTTAATTAAT 3360
 Oy 3361 TGTGATATATCAAAACATTAATCAATTAATGATTTTGTGATTAATTAATGAGCAATTC 3420
 Db 3361 TGTGATATATCAAAACATTAATCAATTAATGATTTTGTGATTAATTAATGAGCAATTC 3420
 Oy 3421 ATGACAGGACACAGACAGCTATTAATCTATCTGAGACTTAATGATTAATCAATTC 3480
 Db 3421 ATGACAGGACACAGACAGCTATTAATCTATCTGAGACTTAATGATTAATCAATTC 3480
 Oy 3481 TTTGAAAAGAGATTTTACAAATATGATCAATTTGGGAGAAATGAGATTTGATTTAT 3540
 Db 3481 TTTGAAAAGAGATTTTACAAATATGATCAATTTGGGAGAAATGAGATTTGATTTAT 3540
 Oy 3541 TTTGCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
 Db 3541 TTTGCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600

Oy 3601 AGAGCATTCATAGAGAGAGGTTTTCAATTTGGTGTGACACCTGTGCTATTCAGTCAAG 3660
 Db 3601 AGAGCATTCATAGAGAGAGGTTTTCAATTTGGTGTGACACCTGTGCTATTCAGTCAAG 3660
 Oy 3661 CAAGCTTACCTGACCTTCCAGATATAAATGATGCTACAGAGCTCTCTTAAAGATGCTTA 3720
 Db 3661 CAAGCTTACCTGACCTTCCAGATATAAATGATGCTACAGAGCTCTCTTAAAGATGCTTA 3720
 Oy 3721 ATTCATTCCTGAGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780
 Db 3721 ATTCATTCCTGAGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780
 Oy 3781 GCTGACCTTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3840
 Db 3781 GCTGACCTTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3840
 Oy 3841 TTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900
 Db 3841 TTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900
 Oy 3901 TCAATGAAAATGAAACACAGAGTGTGCTGATGATTTTGGGGATAGCTGATCTT 3960
 Db 3901 TCAATGAAAATGAAACACAGAGTGTGCTGATGATTTTGGGGATAGCTGATCTT 3960
 Oy 3961 TTAAGGATGCTTTCATCATATTTGCTGAGACACCTGACCAAGATGATCAGCTGATTC 4020
 Db 3961 TTAAGGATGCTTTCATCATATTTGCTGAGACACCTGACCAAGATGATCAGCTGATTC 4020
 Oy 4021 TCAATGAAAATGAAACACAGAGTGTGCTGATGATTTTGGGGATAGCTGATCTT 4080
 Db 4021 TCAATGAAAATGAAACACAGAGTGTGCTGATGATTTTGGGGATAGCTGATCTT 4080
 Oy 4081 AAACACCTCCTCATTGATGATGCTGAGACATGATGATGATGATGATGATGATGATGAT 4140
 Db 4081 AAACACCTCCTCATTGATGATGCTGAGACATGATGATGATGATGATGATGATGATGAT 4140
 Oy 4141 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4200
 Db 4141 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4200
 Oy 4201 ATGTTCTGACGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4260
 Db 4201 ATGTTCTGACGATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4260
 Oy 4261 AAAAAAA 4266
 Db 4261 AAAAAAA 4266
 RESULT 4
 ID AN021004 standard: cDNM, 3416 bp.
 AC AN021004:
 XX 20-MAY-1992 (first entry)
 DT bek receptor protein gene.
 DB bek receptor protein gene.
 XX Fibroblast growth factor receptor, heparin binding proteins.
 KM tyrosine kinase: bacterially expressed kinase; CSF-1; PDGF; ss.
 OS Homo sapiens.
 XX Key
 DT b23486
 FT CDS
 FT /feature
 FT /product= bek receptor protein
 PN M09200999-A.
 XX 23-JAN-1992.

1653 GCGAGGGCTCTCGAGTATGAACTTCAGAGAGACCCAAATGSGAGTTTCCAGAGATTA 1712
 1560 GGGAGGGGCTCTCGAGTATGAACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1619
 1713 GCTGACACTGAGGAGAGCCCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1772
 1620 GCTGACACTGAGGAGAGAGCCCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679
 1713 AGTGGCAATTGACAAAGACAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1832
 1680 AGTGGCAATTGACAAAG 1739
 1833 AGATGATGCCACAGAGAAAGACCTTCCTGATGATGATGATGATGATGATGATGAT 1892
 1740 AGATGATGCCACAGAGAAAGACCTTCCTGATGATGATGATGATGATGATGATGAT 1799
 1893 GATGGGAAACAGAAATATGATTAATCTTCTGAGAGCTGACAGAGATGAGGCTCT 1952
 1800 GATGGGAAACAGAAATATGATTAATCTTCTGAGAGAGAGAGAGAGAGAGAGAGCT 1859
 1953 CTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2012
 1860 CTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1919
 2013 GCGACCGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2072
 1920 GCGACCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1979
 2073 CAAGGACTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2132
 1980 CAAGGACTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2039
 2133 AAATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2192
 2040 AAATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2099
 2193 GAAATGACAGCTTTGAGTACCTGCGAGAGATTCACAAATATATGACTATTCAGAAAGAC 2252
 2100 GAAATGACAGCTTTGAGTACCTGCGAGAGATTCACAAATATATGACTATTCAGAAAGAC 2159
 2253 CACCAATGGGGGCTTCCAGTCAAGAGATGATGATGATGATGATGATGATGATGATGAT 2312
 2160 CACCAATGGGGGCTTCCAGTCAAGAGATGATGATGATGATGATGATGATGATGATGAT 2219
 2313 CACTCATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2372
 2220 CACTCATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2279
 2373 GGGCTGCGCTTACCCAGAGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2432
 2280 GGGCTGCGCTTACCCAGAGATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2339
 2433 GAGATTCGATTAATGACAG 2492
 2340 GAGATTCGATTAATGACAG 2399
 2493 GATGACAGTGGCTTCCAG 2552
 2400 GATGACAGTGGCTTCCAG 2459
 2553 TCTGACTTCGACAAAG 2612
 2460 TCTGACTTCGACAAAG 2519
 2613 AACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2672
 2520 AACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2579
 2673 AGAGCCCATGCTTACAG 2732
 2580 AGAGCCCATGCTTACAG 2639

2733 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2792
 2640 AACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2699
 2733 TACAG 2852
 2700 TACAG 2759
 2853 GAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2912
 2760 GAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2819
 2913 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2972
 2820 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2879
 2973 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3032
 2880 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2939
 3033 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3092
 2940 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2999
 3093 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3152
 3000 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3059
 3153 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3212
 3060 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3119
 3213 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3272
 3120 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3179
 3273 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3332
 3180 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3239
 3333 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3392
 3240 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3299
 3393 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3452
 3300 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3359
 3453 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3509
 3360 TAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3416

RESULT 5
 AB61834
 ID AB61834 standard; DNA: 3244 BP.
 AB61834:
 15-MAY-2002 (first entry)
 Colton adenocarcinoma related gene sequence SEQ ID NO:171.
 Human: cancer: colon: breast: ovary: oesophagus: kidney: thyroid:
 lung: prostate: pancreas: glioma: leukemia: lymphoma: cancerous:
 cytotoxic: gene therapy: anti-neoplastic: Wilms' tumour: adenocarcinoma:
 gene: ds.
 Homo sapiens.
 W0200194629-A2.
 XX
 XX
 XX
 13-DEC-2001.


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Db 1021 ACSTCTCTGGCGGTAATCTATATGGGAAATACCTTACTCTCATGCTGATGGACGTTCTC 1080
Oy 1354 CCGAGGCTCGGAGAGAAAGGAAATATTCAGCTCCCGACAGTACCTGGAGATACCAT 1413
Db 1081 CCGAGGCTCGGAGAGAAAGGAAATATTCAGCTCCCGACAGTACCTGGAGATACCAT 1140
Oy 1414 TATCTCATAGGGGTCTCTTATATGCTGATGAGGATATATCATCTCTGGCCATG 1473
Db 1141 TATCTCATAGGGGTCTCTTATATGCTGATGAGGATATATCATCTCTGGCCATG 1200
Oy 1474 AAGAAACGACAAAGACCAAGCTTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1533
Db 1201 AAGAAACGACAAAGACCAAGCTTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Oy 1534 GGTATCCCTCTGGAGAGAGAGTAAAGATTTCTGAGTATGACAGTCTCTGATACAGC 1593
Db 1261 GGTATCCCTCTGGAGAGAGAGTAAAGATTTCTGAGTATGACAGTCTCTGATACAGC 1320
Oy 1594 AACACCCGCTGGTGGATTAACAAAGGCTCTCTTCAAGAGAGAGAGAGAGAGAGAG 1653
Db 1321 AACACCCGCTGGTGGATTAACAAAGGCTCTCTTCAAGAGAGAGAGAGAGAGAGAG 1380
Oy 1654 GCAGGGGTCTCGAGTATGAACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1713
Db 1381 GCAGGGGTCTCGAGTATGAACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Oy 1714 CTGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1773
Db 1441 CTGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Oy 1774 GTGGGATATGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1833
Db 1501 GTGGGATATGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Oy 1834 GATGATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1893
Db 1561 GATGATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Oy 1894 ATGGGAAACACAGAGATATCTAAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAG 1953
Db 1621 ATGGGAAACACAGAGATATCTAAATCTCTGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Oy 1954 TATGTCATAGTATGATGCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2013
Db 1681 TATGTCATAGTATGATGCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Oy 2014 CCACCGCGGATGAGTACTCCATAGCACTTAAACGCTCTCTGAGAGAGAGAGAGAG 2073
Db 1741 CCACCGCGGATGAGTACTCCATAGCACTTAAACGCTCTCTGAGAGAGAGAGAGAG 1800
Oy 2074 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2133
Db 1801 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Oy 2134 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2193
Db 1861 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Oy 2194 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2253
Db 1921 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Oy 2254 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2313
Db 1981 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Oy 2314 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2373
Db 2041 AAGGACTTGGTGTCACTACGCTACGAGTGGCGAGAGAGAGAGAGAGAGAGAGAGAG 2100
Oy 2374 GAGTCCGCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2433

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Db 2101 GAGTCCGCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Oy 2434 AGAATGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2493
Db 2161 AGAATGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Oy 2494 CAGTATGAGTCCGCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2553
Db 2221 CAGTATGAGTCCGCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Oy 2554 CTGATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2613
Db 2281 CTGATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Oy 2614 CTGATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2673
Db 2341 CTGATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Oy 2674 GAGCCGCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2733
Db 2401 GAGCCGCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
Oy 2734 ACATGCA 2739
Db 2461 ACATGCA 2466

RESULT 7
AA014850
ID AA014850 standard; DNM: 2676 BP.
AC AA014850:
XX 18-FEB-1992 (first entry)
XX 18-FEB-1992 (first entry)
XX Clone PMB1284 encoding complete FGF receptor.
XX Human: fibroblast growth factor; cancer; ss.
XX Homo sapiens.
XX OS
XX Key
XX CDS 23..2534
XX /tag= a
XX W09117183-A.
XX FD
XX 14-NOV-1991.
XX 25-APR-1991; 91MO-JP00557.
XX 28-DEC-1990; 90JP-0415801.
XX 27-APR-1990; 90JP-0113146.
XX 31-JUL-1990; 90JP-0204438.
XX 14-SEP-1990; 90JP-0245256.
XX (TAKE ) TAKEIDA CHEMICAL IND RK.
XX P1
XX Igarashi K, Senoo M, Watanabe T:
XX WPI: 1991-353723/48.
XX P-PSDB; AARI5268.
XX DR
XX New muten(s) of proteins - with fibroblast growth factor
XX receptor activity, useful for treating multiple endocrine
XX neoplasia, prostatic hypertrophy, used for diagnosis
XX PT
XX Example 3: Fig 7: 88pp: English.
XX PS
XX A cDNA library prepared from human cancer cell line Kato III mRNA
XX CC was screened with an oligonucleotide corresponding to amino acids
XX 579-541 of chicken basic FGF receptor. Three positive clones were
XX obtained. One was cloned into pUC119/119 to give pmB1229 (see

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AA014449). The complete FGF coding sequence was obtained by ligating
the insert from pPB1229 to the DNA sequence of the plasmid pPB3281
insert which encodes the carboxyl terminus of the FGF receptor from
Glu 533 onwards.

SQ Sequence 2676 BP; 743 A; 645 C; 738 G; 550 T; 0 other.

Query Match	51.3%;	Score 2188;	DB 12;	Length 2676
Post (cont) similarity	06.0%;	Prod NO. 0;		

Matches 2259; Conservative 0; Mismatches 60; Indels 15; Gaps 2.

oy 250 GGACCGGGGATTCGTACCGTAACCATGGTCAAGCTGGGGTCGTTCAATCAGCCCTGGT

QY	310	GTACCCATGGCAACCTCTTCCCTGGCCGCGCCCTCTTCACTTAACTTGAAGATACACCA	369
Dp	61	GTTCACATATGCAACCTCTTCCCTGGCCGCGCCCTCTTCACTTAACTTGAAGATACACCA	120
QY	370	TTTAGAGCGAAGAAAGGCGACACACCAATACCAATCTCTACACGCAAGTGTACTGGCT	429
Dp	121	TTTAGAGCGAAGAAAGGCGACACCAATACCAATCTCTACACGCAAGTGTACTGGCT	180
QY	430	CGCGACGGGGAATCGCTGAAGAGTGGGCTCCCTCTTGGAAGAGTGGCGCCGTGATCAATGG	489
Dp	181	CGCGACGGGGAATCGCTGAAGAGTGGGCTCCCTCTTGGAAGAGTGGCGCCGTGATCAATGG	240
QY	490	ACTGACGAGTGGTGCCTCTGGGGGGCCCAATAGGAGTCTATTGGGGAGTACTTGG	549
Dp	241	ACTGACGAGTGGTGGCTCTGGGGGGCCCAATAGGAGTCTATTGGGGAGTACTTGG	300
QY	550	CAGTAAAGGGGCGCCACGCTTGAAGATCTCGGCGCTCTATGCTTTACTCGCATGACACT	609
Dp	301	CAGTAAAGGGGCGCCACGCTTGAAGATCTCGGCGCTCTATGCTTTACTCGCATGACACT	360
QY	610	GTGACAGTATGAATCTGTGTACTTCAATGGAAATGTACAGAAATGCTATCCGGAAT	669
Dp	361	GTGACAGTATGAATCTGTGTACTTCAATGGAAATGTACAGAAATGCTATCCGGAAT	429
QY	670	GATGAGATGACACCGCATGTGTGGGAAGATTTTGTCAATGATGAACAGTAAACAAGAA	729
Dp	421	GATGAGATGACACCGCATGTGTGGGAAGATTTTGTCAATGATGAACAGTAAACAAGAA	480
QY	730	GCACATATCTGAGCAACAGCAAGAAATATGGAAAGGCGCTCTCAATGTGTGGCGGCG	789
Dp	481	GCACATATCTGAGCAACAGCAAGAAATATGGAAAGGCGCTCTCAATGTGTGGCGGCG	540
QY	790	AACACTGTCAACTTTCGCTGCGCACAGCGGGGGGAGACCCATATCCAACTGCGGTGGCTG	849
Dp	541	AACACTGTCAACTTTCGCTGCGCACAGCGGGGGGAGACCCATATCCAACTGCGGTGGCTG	600
QY	850	AAAAAGGGGAAGAGATTTAACAGAGACATCGCATTTGAGAGGCTCAAGGTACCAACACG	909
Dp	601	AAAAAGGGGAAGAGATTTAACAGAGACATCGCATTTGAGAGGCTCAAGGTACCAACACG	660
QY	910	CACGTGACCTCTAATTGTAAGAAATGTGTCTCCATCTGCAACAGGAATTTATACCTGTGTG	969
Dp	661	CACGTGACCTCTAATTGTAAGAAATGTGTCTCCATCTGCAACAGGAATTTATACCTGTGTG	720
QY	970	GAGTCAGATCAATTAATGGGTGTGCATCAATGTGTCTGCATCTGGAAGAGGAATTTACCTGTGTG	1029
Dp	721	GAGTCAGATCAATTAATGGGTGTGCATCAATGTGTCTGCATCTGGAAGAGGAATTTACCTGTGTG	780
QY	1030	CGCTACCGGCGCCATCTCCCAAGCGCGAGCTGCGGCAAAATCCCTCCACAGTGGTGTGAGGA	1089
Dp	781	CGCTACCGGCGCCATCTCCCAAGCGCGAGCTGCGGCAAAATCCCTCCACAGTGGTGTGAGGA	940
QY	1090	GACGTGAGTATTTCTGCGAAGCTTTTAACTGATACCGCGCGACCGCAATCGATGATCAAG	1149
Dp	841	GACGTGAGTATTTCTGCGAAGCTTTTAACTGATACCGCGCGACCGCAATCGATGATCAAG	900
QY	1150	CACGTGAGTATTTCTGCGAAGCTTTTAACTGATACCGCGCGACCGCAATCGATGATCAAG	1209

[illegible]

2281 ATGGCTCAGAAAGCCCTTTGATGATGATATACACTCATCAGATGATCTGTGCTCTTC 2340
 2035 ATGGCTCAGAAAGCCCTTTGATGATGATATACACTCATCAGATGATGATGATGCTCTTC 2094
 2341 GGGGCTTAATGATGGAGATCTTCACTTTAGGGGCTGGCCCTACCCAGGATATCCCTTC 2400
 2095 GGGGCTTAATGATGGAGATCTTCACTTTAGGGGCTGGCCCTACCCAGGATATCCCTTC 2154
 2401 GAGCACTTTTAAGCTCTGAGCAAGCAAGCAAGATGATAGCAAGCAAGCAAGCAAGCAAG 2460
 2155 GAGCACTTTTAAGCTCTGAGCAAGCAAGCAAGATGATAGCAAGCAAGCAAGCAAGCAAG 2214
 2461 AAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
 2215 AAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2274
 2521 TTCAAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2574
 2275 TTCAAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2328

RESULT 8
 AA014849
 24014849 standard: DNA: 1954 BP.
 AA014849:
 18-FEB-1992 (first entry)
 Clone pPB1229 encoding protein with FGF receptor activity.
 Human: fibroblast growth factor; cancer; ss.
 Homo sapiens.
 Key
 Location/Qualifiers
 CDS
 25..1953
 /tag= a
 WO9117183-A.
 14-NOV-1991.
 25-APR-1991. 91WO-JP00557.
 28-DEC-1990. 50JP-0415801.
 31-APR-1990. 50JP-0113148.
 31-APR-1990. 50JP-0113148.
 14-SEP-1990. 90JP-0245256.
 (TAKE) TAKEEDA CHEMICAL IND KK.
 Igarashi K, Senoo M, Watanabe T.
 WPI: 1991-35373/48.
 P-PSDB: ARI15267.
 New nuclein(s) of proteins - with fibroblast growth factor
 receptor activity, useful for treating multiple endocrine
 neoplasia, prostatic hyperplasia, used for diagnosis
 Example 2: Fig 4: 88pp: English.
 A cDNA library prepared from human cancer cell line Kato III mRNA
 was screened with an oligonucleotide corresponding to amino acids
 529-541 of chicken basic FGF receptor. Three positive clones were
 obtained. One was cloned into pUC118/119 to give pPB1228. The
 sequence of pPB1229 was the longest of the three clones. See AA014848
 and pPB1228 and which lacks nucleotides 134-478 and 1309-1314 of
 pPB1229 and pPB1228. The amino acid sequence of the protein
 corresponding to nucleotide 1029 of pPB1225.

SQ Sequence 1954 BP: 531 A: 481 C: 544 G: 398 T: 0 other:
 Query Match 42.6%; Score 1817.2; DB 12; Length 1954;
 Best Local Similarity 56.3%; Pred. No. 0;
 Matches 1887; Conservative 0; Mismatches 58; Indels 15; Gaps 2;
 250 GAGCGGGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 309
 1 GAGCGGGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 310 GTACACATGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 369
 6 GTACACATGACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 370 TTGAGGCGAAG 429
 121 TTGAGGCGAAG 180
 430 GGGCGAGGAG 489
 181 GGGCGAGGAG 240
 490 ACTAAG 549
 241 ACTAAG 300
 550 CAGATTAAG 609
 301 CAGATTAAG 360
 610 GTGACACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 669
 351 GTGACACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 670 GATGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 729
 421 GATGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789
 730 GATGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 849
 481 GATGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 790 AACACTGAT 849
 541 AACACTGAT 600
 850 AAAAAGCGGAG 909
 601 AAAAAGCGGAG 660
 910 CACTGAG 969
 661 CACTGAG 720
 970 GTGAG 1029
 721 GTGAG 780
 1030 GTGAG 1089
 781 GTGAG 840
 1090 GACGTGAG 1149
 841 GACGTGAG 900
 1150 GACGTGAG 960
 901 GACGTGAG 960
 1210 AAGCGCGCGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1269
 961 AAGCGCGCGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014

Qy	1270	ACGTTGAGAGCGGTGGGAAATATGAGTCGTGTGGCGGATATCATTTGGGATATCTT	1329
Dy	1015	ACGGAGCGGATAGCGGGGGAATATATATGTGTAAAGCTCTCCAAATATATATAGGCGAAGCCAAAC	1074
Qy	1330	CTCTGTCGATGCTTGAACAGAGTCTGCC-----ACGCGTGGAGAGAAAGAGCAAT	1380
Dy	1075	CAGCTGCTGCTGGCTGCTATGTCTCTGAATAACGAAACGCGCTGAGAGAAAGAAAGCAAT	1134
Qy	1381	ACAGCTTGTCCGAGATACAGTGGAGATAGAGCAATTTACAGTATAGAGGATCTTCTTAATGCGC	1440
Dy	1135	ACAGCTTGTCCGAGATACAGTGGAGATAGAGCAATTTACAGTATAGAGGATCTTCTTAATGCGC	1194
Qy	1441	TCGTATGCTGTACAGATCATCTGTGCGCAATGAGAACAGCAACAGACAGCAATCTG	1500
Dy	1195	TCGTATGCTGTACAGATCATCTGTGCGCAATGAGAACAGCAACAGACAGCAATCTG	1254
Qy	1501	ACAGCAACGCGCGCTGTGGCAAGATGTACCAAAACGATATCCCGCGGAGAACAGATACAA	1560
Dy	1235	ACAGCAACGCGCGCTGTGGCAAGATGTACCAAAACGATATCCCGCGGAGAACAGATACAA	1314
Qy	1561	GTTTTCGGGTATGTCACAGCTCTCTCTCAATATCCAGCAACCCGCGGTGACGATACAAACA	1620
Dy	1315	GTTCGTCTCTTGAAGAGCAACGATCCGATAGCGAGGGGTCTCGAGATATACATACAA	1680
Qy	1621	CGCTCTCTTGAAGAGCAACGATCCGATAGCGAGGGGTCTCGAGATATACATACAA	1680
Dy	1375	CGCTCTCTTGAAGAGCAACGATCCGATAGCGAGGGGTCTCGAGATATACATACAA	1434
Qy	1681	GAGGACCCAAATGCGGATCTCCAAAGATTAAGCTGACAGCTGGCAACCCCTGGGAGAA	1740
Dy	1435	GAGGACCCAAATGCGGATCTCCAAAGATTAAGCTGACAGCTGGCAACCCCTGGGAGAA	1494
Qy	1741	GGTTGGTTGGGCAATGTGTCTATGGCGGAAACAGATGGATATTTGACAAAGCAAGCCAAAG	1800
Dy	1495	GGTTGGTTGGGCAATGTGTCTATGGCGGAAACAGATGGATATTTGACAAAGCAAGCCAAAG	1554
Qy	1801	GAGGCGGTGACAGCTGGCGGTGAAGATGTTGAAAGATGATGATCCAGCAACAAACAACTTCT	1860
Dy	1555	GAGGCGGTGACAGCTGGCGGTGAAGATGTTGAAAGATGATGATCCAGCAACAAACAACTTCT	1614
Qy	1861	GATCTGTGTCTGACAGATGAGATGAGATGAGATGATGATGATGATGATGATGATGATGAT	1920
Dy	1615	GATCTGTGTCTGACAGATGAGATGAGATGAGATGATGATGATGATGATGATGATGATGAT	1570
Qy	1921	CTCTCTTGACCTGACAGCAACAGATGAGGAGCTCTGTATGTACATAGTTAGCTATGACCTTAA	1980
Dy	1675	CTCTCTTGACCTGACAGCAACAGATGAGGAGCTCTGTATGTACATAGTTAGCTATGACCTTAA	1734
Qy	1981	GGCAACCTCGAGATACCTGTGAGACCGGACAGCGCAAGCGGATAGCATACGTCTATGAC	2040
Dy	1735	GGCAACCTCGAGATACCTGTGAGACCGGACAGCGCAAGCGGATAGCATACGTCTATGAC	1794
Qy	2041	ATTTAACCGTGTCTGTGAGAGACAGATACATCTTAAGAGAGCTGTGTGTATGACAGCTACAG	2100
Dy	1795	ATTTAACCGTGTCTGTGAGAGACAGATACATCTTAAGAGAGCTGTGTGTATGACAGCTACAG	1854
Qy	2101	CTTGCGCCACAGCATGCGATCTTGCTGCTCAAAATGTATTCATGCAATATGACAGCC	2160
Dy	1855	CTTGCGCCACAGCATGCGATCTTGCTGCTCAAAATGTATTCATGCAATATGACAGCC	1914
Qy	2161	AGAAATGTTTTGTGATACAGAAACAATGTGTGAGAAATATG	2200
Dy	1915	AGAAATGTTTTGTGATACAGAAACAATGTGTGAGAAATATG	1954

RESULT 9	
AAQ14851	
ID	AAQ14851 standard; DNA: 2310 BP
XX	
AC	AAQ14851;
XX	
DT	18-FEB-1992 (first entry)

Qy	2153	CGGAAATGTTTGGTACGAGAAACAAGTGAATGAAATAGCAGACTTGGATCGCA	2218
Dy	1562	CGAAGAAATGTTTGGTGAACAAACATGATGAATAGCAGACTTGGATCGCA	1623
Qy	2213	GAGATTAATGTTTGAATACATATTCACAAAGCCGCAAGCCGGCGCTTCAGTCACT	2278
Dy	1623	GAGATTAATCAACAATATACACTATTCACAAAGCCGCAAGCCGGCGCTTCAGTCACT	1681
Qy	2278	GAGATGCTCGAAGAACCCCTGTTTGATAGAGATACACTCATGATGATGCTGGCTCT	2343
Dy	1682	GAGATGCTCGAAGAACCCCTGTTTGATAGAGATACACTCATGATGATGCTGGCTCT	1741
Qy	2333	TCCGGGGCTGTAATCCGCAATCTTCACATTTAGCGGGCTGGCGCTTACCAGGATTCGG	2398
Dy	1742	TCCGGGGCTGTAATCCGCAATCTTCACATTTAGCGGGCTGGCGCTTACCAGGATTCGG	1801
Qy	2398	TGGGAGAACTTTTAAAGCTCCTGAAAGGAGACACAGATGGAATAGCCAGCAATGCA	2458
Dy	1802	TGGGAGAACTTTTAAAGCTCCTGAAAGGAGACACAGATGGAATAGCCAGCAATGCA	1861
Qy	2458	CGACGAGACCTTTAAAGTCTGCTAAGGAGATGTCGCATGCAATGCTCCGACGAGCA	2518
Dy	1862	CGACGAGACCTTTAAAGTCTGCTAAGGAGATGTCGCATGCAATGCTCCGACGAGCA	1922
Qy	2518	CGTTTCAGCAGAGTGGTAAAGAGACTTGGATGATCATTTCTCACTCTACAAACCATGAG	2574
Dy	1922	CGTTTCAGCAGAGTGGTAAAGAGACTTGGATGATCATTTCTCACTCTACAAACCATGAG	1977
RESULT 10			
AA014049	ID		
AA014049	standard; cDNA; 2345 bp.		
AA014049:			
AC	37-DRC-2001	(updated)	
AC	09-JAN-1992	(first entry)	
DT	Human ect gene.		
DE	Keratinocyte growth factor receptor; KGF; tyrosine kinase; ss.		
Kw	Homo sapiens.		
XX	Key	location/Qualifiers	
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FT	mat-peptide	250..2307	
FT	/*tag- b		
FT	s19-peptide	187..249	
XX	/*tag- c		
PN	USM560035-N.		
XX	10-SEP-1991.		
XX	09-AUG-1990:	90US-0560035.	
XX	09-AUG-1990:	90US-0560035.	
XX	(USSH) NMT INST OF HEALTH.		
XX	MIKI T, Aarson SA, Fleming T;		
PI	WPI: 1991-310282/42.		
DR	P-PSDB: AARI4280.		
XX	New genetic cloning vectors - which provide efficient, automatic		
PT	directional cloning of cDNA copy of a eukaryotic mRNA.		
PS	Disclosure: Fig 15; 108pp; English.		
XX	The sequence was obtd. from a clone isolated from a cDNA library		

Db	1083	CAATTTTATTTGGGAGGCGAACACAGCTCTGCGTGCCTGAGCTGCCTCCATGAGAA	1142
Qy	1368	-----AGAAAGAGATTACAGTTTCCCAACAGTCCGATATGACGATTTTGGCAT	1421
Db	1143	AATGATGAACAGGAGACATGATATCATCATGAGATATAGGAAATGCGCATCTACTGTGT	1202
Qy	1422	AGGGGTCTTCTTAAATCCGTCGTATGAGTGTATACAGTATATCTGCTCGAATGAGAAAC	1481
Db	1203	GGAGAGCTTCCTGATACCTGACATATGAGATGATGATGATGATGATGATGATGATGATG	1262
Qy	1482	GAGCAAGACGACAGCTTACAGCAGCGGCTGTGACAGTGCAGTGCAGTGCAGTGCAGTGC	1541
Db	1263	AGCGAAGAGGTGACCTTACAGAGCCGACCCGCTGTGCACAGTGTAGCAAGATGTCGCC	1322
Qy	1542	CGTCGCGAGACAGATAGTATTCGGCTGAGTGCAGGTCTGCAGTAAGATCCACACGCC	1601
Db	1323	CGTCGCGAGACAGATAGTATTCGGCTGAGTGCAGGTCTGCAGTAAGATCCACACATCC	1382
Qy	1602	GGTGTGGAGATGATACAGACAGCTCTCTGTATGACAGGACAGCCGATGTGTGGAGGGT	1661
Db	1383	ACGTGTCGGATGACATGCTGCTGTCTTCCAAACATGACACCACTTGTGTGGCGGGGT	1442
Qy	1662	CTTCGAGATGAACTTCCAGAGACCCAAAATGGAGATTCCAAAGATTAACGTGACACT	1721
Db	2163	ATACCCCTGAAATTCAGATGTAAGAAGATCTTTCACAGCTCTCTTAAGAGAGCCACCAATG	2201
Qy	2222	TAAAGCAGCAATCTCCACCAAGCAATCTGATACATATGATATGAGGATCTGTGGATCCAT	2301
Db	2223	CAGCTGTCCAGCTGACATGATGATATATGATATATGATATATGATATATGATATATGAT	2282
Qy	2350	GGCTGTCCAGAGACCACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATG	2861
Db	2283	GGCTGTCCAGAGACCACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATG	2342
Qy	2362	CACACCAATGAGATTAAGTATGAGACCTGACCAACAGCTTCCAGATATTCAGTATGATTA	2621
Db	2343	AACATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2402
Qy	2622	CCGTGAGACAAAGAGTCTTCTGCTTCAAGAGATGATGATGATGATGATGATGATGATG	2681
Db	2403	TCCGATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2462
Qy	2682	GGCTTACAGACACTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	2739
Db	2463	GGCTTACAGACACTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	2520

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Job time : 598 secs

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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:57:41 : Search time 99 seconds

(without alignments)
13221.176 Million cell updates/sec

Title: US-09-954-556-3

Sequence: 4268 1 cccagagccacatcttcgc.....acttaaaaaaaaaa 4268

Scoring table: IDENTITY, NUC

Gapop 10.0, Capext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents, NA : *

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- 2: /cgn2.6/pdata/1/jna/5B.COMB.seq.*
- 3: /cgn2.6/pdata/1/jna/5C.COMB.seq.*
- 4: /cgn2.6/pdata/1/jna/6B.COMB.seq.*
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- 6: /cgn2.6/pdata/1/jna/Backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3386.6	75.3	3418	US-08-451-822A-15	Sequence 15, Appl
2	3190.2	51.3	2676	US-08-423-430-15	Sequence 15, Appl
3	1817.2	42.6	1954	US-08-471-570-5	Sequence 9, Appl
4	1692.8	35.7	2310	US-08-471-570-5	Sequence 9, Appl
5	1367.6	33.0	2675	US-08-070-165F-5	Sequence 5, Appl
6	1367.6	33.0	2675	US-08-885-418-5	Sequence 5, Appl
7	1318.8	36.9	1603	US-08-471-570-3	Sequence 9, Appl
8	1318.8	36.9	1603	US-08-885-418-5	Sequence 5, Appl
9	1276.4	26.9	2681	US-08-423-430-15	Sequence 15, Appl
10	1276.4	26.9	2681	US-08-885-418-5	Sequence 5, Appl
11	1182.2	27.7	2469	US-07-997-113-2	Sequence 1, Appl
12	1182.2	27.7	2469	US-08-459-296-1	Sequence 1, Appl
13	1182.2	27.7	2469	US-07-997-113-2	Sequence 2, Appl
14	1180.6	27.7	2662	US-08-451-822A-14	Sequence 14, Appl
15	1180.6	27.7	2662	US-08-323-430-14	Sequence 14, Appl
16	1150.6	27.3	2733	US-08-423-430-15	Sequence 15, Appl
17	1150.6	27.3	2733	US-08-885-418-5	Sequence 5, Appl
18	1141	26.7	3503	US-07-631-217A-14	Sequence 1, Appl
19	1141	26.7	3503	US-08-166-717D-1	Sequence 1, Appl
20	981.8	23.0	5993	US-09-383-630-1	Sequence 1, Appl
21	981.8	23.0	5993	US-09-383-630-2	Sequence 2, Appl
22	961.8	22.5	2043	US-09-099-749-10	Sequence 10, Appl
23	956.2	22.4	8083	US-09-383-630-4	Sequence 4, Appl
24	956.2	22.4	8083	US-09-383-630-5	Sequence 5, Appl
25	931.6	21.8	1079	US-08-421-570-13	Sequence 13, Appl
26	623.2	14.6	1875	US-08-070-165F-3	Sequence 3, Appl
27	623.2	14.6	1875	US-08-885-418-3	Sequence 3, Appl

28	623	14.6	1839	US-08-070-165F-7	Sequence 7, Appl
29	623	14.6	1839	US-08-885-418-7	Sequence 7, Appl
30	603.4	14.1	1605	US-08-471-570-1	Sequence 1, Appl
31	598.8	14.0	1055	US-08-701-191A-5	Sequence 5, Appl
32	527.5	14.0	933	US-08-701-191A-5	Sequence 11, Appl
33	476.2	10.0	1983	US-08-057-860-18	Sequence 18, Appl
34	426.2	10.0	1983	US-08-057-860-18	Sequence 34, Appl
35	245.4	5.7	4508	US-08-323-474-1	Sequence 1, Appl
36	205	4.8	4138	US-07-906-397A-5	Sequence 1, Appl
37	205	4.8	4138	PCT-US93-06093-1	Sequence 1, Appl
38	197.4	4.6	360	US-08-220-260A-4	Sequence 4, Appl
39	184	4.5	3845	US-07-813-523-3	Sequence 3, Appl
40	182.8	4.5	5406	US-07-946-507-3	Sequence 3, Appl
41	182.8	4.5	5406	US-07-946-507-3	Sequence 34, Appl
42	182.8	4.5	5406	US-08-282-517-5	Sequence 5, Appl
43	182.8	4.5	5406	US-08-282-517-5	Sequence 5, Appl
44	182.8	4.5	5406	US-08-601-891-5	Sequence 5, Appl
45	182.8	4.5	5406	US-08-601-891-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-451-822A-15
Sequence 15, Application US/08451822A
Patent No. 5663888
Inventor: CRONIN, James
Applicant: Cronin, Craig A
Applicant: Cronin, Greg
Applicant: Schlessinger, Joseph
Title of Invention: Fibroblast Growth Factor Receptors
Number of Sequences: 19
Address: 500 Arcola Road
City: Collegeville
State: PA
Country: USA
ZIP: 19426
Computer Readable Form:
Computer File: floppy disk
Operating System: PC-DOS/MS-DOS
Software: PatentIn Release #1.0, Version #1.25
Current Application Data:
Application Number: US/08451, 822A
Filing Date: 26-MAY-1995
Classification: 435
Priority Date: 14-OCT-1994
Filing Date: 14-OCT-1994
Prior Application Number: US 08/323,430
Application Number: US 07/934,372
Filing Date: 21-AUG-1992
Prior Application Data: US 07/549,587
Filing Date: 06-JUL-1990
Attorney/Agent Information:
Name: Sawitzky, Martin
Registration Number: 29,699
Reference/Docket Number: A0496E
Telecommunication Information:
Telephone: (610) 454-1608
Information For SEQ ID NO: 15:
Length: 3416 base pairs
Type: nucleic acid
Strandness: single
Strandness: linear
Molecule Type: cDNA

US-08-451-822A-15

Query Match 79.3%; Score 3386.6; DB 2; Length 3416;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3411; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

93 CCAAGTCCCGAGAGAGCGTCCATTTAGATAGTACGACGACGAGCGGCGTCCG 152
 Db 2 CCAAGTCCCGAGAGAGCGTCCATTTAGATAGTACGACGAGCGGCGTCCG 60
 153 TTCTGAGCCACCGACGAGCGTGAAGGCAATGGCGGTAGTCCATGCCCTGAGGAGAGT 212
 Db 61 TTCTGAGCCACCGACGAGCGTGAAGGCAATGGCGGTAGTCCATGCCCTGAGGAGAGT 119
 213 GCGAGTGGGATTAACTGTCACATGAGATATGGAAGAGCCGGGAAATGGTACCTGAC 272
 Db 120 GCGAGTGGGATTAACTGTCACATGAGATATGGAAGAGAGCCGGGAAATGGTACCTGAC 179
 273 CATGTGACGTGGAGGTGTTCATCTCTGCTGGTGTGTGTCACATGACACCTTGCTCT 312
 Db 180 CATGTGACGTGGAGGTGTTCATCTCTGCTGGTGTGTGTCACATGACACCTTGCTCT 239
 333 GCGCGCGCCCTCTCTGAGTTAGATAGACATACCAATGACGAGACCAACCAAC 392
 Db 240 GCGCGCGCCCTCTCTGAGTTAGATAGACATACCAATGACGAGACCAACCAAC 399
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 Db 300 CAAATACCAATCTCTACACAGAGTTAGTGTGCTGGCGACAGGGAGTCCGTAGAGT 359
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 Db 360 GCGGTGCTGTTGAAGATGCGCGCGACACATGTTGAGACTAAAGATGGGTGCACTGGG 419
 513 GCGCAACATATGACACATGCTTATTTGGGAGTACTTCCAGATTAAGGGGCGCCAGCTT 572
 Db 420 GCGCAACATATGACACATGCTTATTTGGGAGTACTTCCAGATTAAGGGGCGCCAGCTT 479
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 Db 480 AGACTCGGCGCTCTAGTCTTGTACTGCGCATAGAGACTAGACATGTAACCTGTACTT 539
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 Db 600 GGAAGATTTTTGTGACGAGACAGTAAACAAAGAGACCACTACTGTGACCAACAGA 659
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 Db 660 AAGAGTGGAAAGCGGTGCTATGCTGTGCGCGGCAACACATGTAAGTTGCGTACCT 719
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 Db 720 AGCGCGGGGGAACCCCATGSCAACATCTGCGTGGCTGAAAGCGGAAGAGATTTAAACA 779
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 Db 1320 TTATGCTGATGAGGCTCTCTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1379
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 Db 2040 AAAATGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2099


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OY 2193 GAAATTCAGACATTTGGACTGCCAGAGATATCAACATATAGACTATTACAAAAGAC 2252
DB 2100 GAAATTCAGACATTTGGACTGCCAGAGATATCAACATATAGACTATTACAAAAGAC 2159
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DB 2760 GAGTAAATATATGAAAAATATACATATGTGTAAATATTTATACAGTGAACCTG 2819
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OY 3273 CACATATTTCTTAATTTTCAAGACAGAGGTGGAATAATCTTTTCTTCTTCAAGGAAA 3332

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DB 3180 CACATATATTTCTTAATTTTACCAAGAGGTGGAATAATCTTTTCTTCAAGGAAA 3239
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DB 3300 TTTTGTGTATTAATTAATGATGCTATTAAGCAGCAGCAGCAGCAGCTGATTAATAT 3359
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RESULT 2
US-08-323-430-15
Sequence 15: Application US/08323430
Best Local 6.1416
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 15
CORRESPONDING ADDRESS:
ADDRESS: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
STATE: PA
COUNTRY: USA
DATE RECEIVED: 19426
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323, 430
FILING DATE: 06-JUL-1990
PRIORITY INFORMATION:
PRIORITY DATE: 435
PRIORITY APPLICATION: 435
APPLICATION NUMBER: US to be assigned
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/549, 587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Woodman, Roseanne
REFERENCE: 524
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-323-430-15

Query Match 70.3% Score 3386.6 DB 4: Length 3416:
Best Local Similarity 99.8% Freq 0.0:
Matches 3411: Conservative 0: Mismatches 4: Indels 2: Gaps 2:
OY 93 CACAGGTCCGCGAGAGCTGCTCCATTCAGATGAGACGACAGCAGCAGCAGCAGCAGCAG 352
DB 2 CCGAGGTCCGCGAGAGCTGCTCCATTCAGATGAGACGACAGCAGCAGCAGCAGCAGCAGCAG 60
OY 153 TTCTCAAGCCCAAGCAGAGCTGAGATATGAGGTATGCTCACTGCTGTAGAGAAATGT 212

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Db      120 GCACATGGGATTACGTTCCACATGAGAGATTGAGAGAGAGCCGGAGATTGGTACCTGAC 179
Oy      273 CATGTGACGTGGGGTGGTTTCACTGCTGGCTGGTGGTGCACATGACCACTGGTGGCT 332
Db      180 CAGGTGACGTGGGGTGGTTTCACTGCTGGCTGGTGGTGCACATGACCACTGGTGGCT 239
Oy      333 GCGCGGGCGCTGCTGAGTTACGTTACGACATGATGAGCAATGAGACCAACCAAC 392
Db      240 GCGCGGGCGCTGCTGAGTTACGTTACGACATGATGAGCAATGAGACCAACCAAC 299
Oy      393 CAATACCAATCTCTACACAGAAATGCTACGTGGCTGGGCGACAGGAGATGCTACAGCT 452
Db      300 CAATACCAATCTCTACACAGAAATGCTACGTGGCTGGGCGACAGGAGATGCTACAGCT 359
Oy      453 GCGGTGGCTGGTGAAGAGCGCGCTGACAGTTGGTACCTAAGAGATGGGTGACCTGG 512
Db      360 GCGGTGGCTGGTGAAGAGCGCGCTGACAGTTGGTACCTAAGAGATGGGTGACCTGG 419
Oy      513 GCCCAAAATAGGACAGCTCTATTGGGGAGTACCTGCAATGAAGGCGACAGGCTAC 572
Db      420 GCCCAAAATAGGACAGCTCTATTGGGGAGTACCTGCAATGAAGGCGACAGGCTAC 479
Oy      573 AAGACTCGGCGCTCTAGTCTTACTGCGAGTACGAGACTGAGACAGTGAACCTGGTACT 632
Db      480 AAGACTCGGCGCTCTAGTCTTACTGCGAGTACGAGACTGAGACAGTGAACCTGGTACT 539
Oy      633 CATGTGAATGTCAACATGCCATCTCATCCGAGAGATGATGAGATGACACCAATGGTGC 692
Db      540 CATGTGAATGTCAACATGCCATCTCATCCGAGAGATGATGAGATGACACCAATGGTGC 599
Oy      693 GGAAGATTTTGTGAGTGAAGAACATGACAAACAAAGAGACATACGTGACCAACAG 752
Db      500 GGAAGATTTTGTGAGTGAAGAACATGACAAACAAAGAGACATACGTGACCAACAG 659
Oy      753 AAGAGTGAAGAGGAGTGCATGCTGTGCTCGCGGCAACACTGTCAAGTTTCGTGCTCC 812
Db      660 AAGAGTGAAGAGGAGTGCATGCTGTGCTCGCGGCAACACTGTCAAGTTTCGTGCTCC 719
Oy      813 ACCCGGGGGAGACCAATGCGCACATGCGGTGGTGGTGAAGAGAGATTATAC 872
Db      720 ACCCGGGGGAGACCAATGCGCACATGCGGTGGTGGTGAAGAGAGATTATAC 779
Oy      873 GAGCATGCTGATGGAGGTACAGAGTACGAACCAACGACATGGACCTCATATTATGAAG 932
Db      780 GAGCATGCTGATGGAGGTACAGAGTACGAACCAACGACATGGACCTCATATTATGAAG 839
Oy      933 TGTGTGTCCTCATGACAAAGGAAATTATACCTGTGTGGTGAATATATACGGGTGCAT 992
Db      840 TGTGTGTCCTCATGACAAAGGAAATTATACCTGTGTGGTGAATATATACGGGTGCAT 899
Oy      993 CAATCAACAGTACCACTGATATGTTGTGAGACGATGTGCTCCACCGCCCATCTCCAAAG 1052
Db      900 CAATCAACAGTACCACTGATATGTTGTGAGACGATGTGCTCCACCGCCCATCTCCAAAG 959
Oy      1053 CGGACTGTCGGCGAAATGCTCTGACAGTGGTGGAGAGGACATGAGTTGTCTCCAAAG 1112
Db      960 CGGACTGTCGGCGAAATGCTCTGACAGTGGTGGAGAGGACATGAGTTGTCTCCAAAG 1019
Oy      1113 TTACATGATGCCACGCGCCACATCACTGATGATCAACAGCAGTGGAGAAAGACCGCAT 1172
Db      1020 TTACATGATGCCACGCGCCACATCACTGATGATGATCAACAGCAGTGGAGAAAGACCGCAT 1079
Oy      1173 ATACGAGCCCGAGCGGCTGCTACCTCAAGGCTTCAAGAGCGCGCGGTTAAACACAA 1232
Db      1080 ATACGAGCCCGAGCGGCTGCTACCTCAAGGCTTCAAGAGCGCGCGGTTAAACACAA 1139
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Db      1140 GACAAAGAGATTGAGGTGTCTATATTCGGATGTGTAACCTTTGAGAGCGCTGGGAATA 1199
Oy      1293 TACGTGCTTGGCGGGGTAAATTCATTTGGGATATTCCTTACCTGTGATGTGTAACATCTT 1352
Db      1200 TACGTGCTTGGCGGGGTAAATTCATTTGGGATATTCCTTACCTGTGATGTGTAACATCTT 1259
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Db      1260 GCGAGCGCTTGGAAGAAAGAGATATACGCTTTCCTCCACATGCTACGTGAGATAGCAT 1319
Oy      1413 TTACATGATAGGGGTCTCTTATATCCCTGTATGTGTGTGAACAGTCACTGTGTCCGAAT 1472
Db      1320 TTACATGATAGGGGTCTCTTATATCCCTGTGTATGTGTGTGAACAGTCACTGTGTCCGAAT 1379
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Db      1380 GAGAGACAGACAAAGACGACAGCTTACACACACACCGGCTGTGACACAGCTGACAA 1439
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Db      1440 AGTATCCCTCGCGAGAACAGATGACAGTTTGCGGTAGTACGACTCTCTCATGATCT 1499
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Db      1500 CAACACCCCGCTGTGTGAGATACACACACCTCTGTCAACAGGACACCCCATCT 1559
Oy      1653 GCGAGCGCTTCCGAGTATGAACTTCAGAGAGACCCAAATGGAGATTGCCAAAGATTA 1712
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Db      1620 GCTGACACTGGGCAAGCCCTGTGGAGAAAGATTGCTTTGGGGCAATGGGTCAATGGGAGAG 1679
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Db      1680 ACTGGGATGAGAAAGACACAGCCGAGACAGCGGCTACAGTGGCTGTGAGATGTGGA 1739
Oy      1833 AGATGATGCCACAGAGAAAGACCTTTCTGATCTGTGTGTACAGATGAGATGATGAAT 1892
Db      1740 AGATGATGCCACAGAGAAAGACCTTTCTGATCTGTGTGTGTACAGATGAGATGATGAAT 1799
Oy      1893 GATTGGGAACAGAAATATCATAAATCTTTGGAGGCTGTGCAACAGATGGCGCTCT 1952
Db      1800 GATTGGGAACAGAAATATCATAAATCTTTGGAGGCTGTGCAACAGATGGCGCTCT 1859
Oy      1953 CTATGCTATAGTTGAGTATGCTCTCTTAAAGCCAACTCTCGAATATACCTCGAGCCGAG 2012
Db      1860 CTATGCTATAGTTGAGTATGCTCTCTTAAAGCCAACTCTCGAATATACCTCGAGCCGAG 1919
Oy      2013 GCGCACCGGGAGAGAGTCTCTATGCAATATTAACCGCTGTCTGAGAGAGAGATGACAT 2072
Db      1920 GCGCACCGGGAGAGAGTCTCTATGCAATATTAACCGCTGTCTGAGAGAGAGATGACAT 1979
Oy      2073 CAAGGACTTGTGTGATGACACTACACAGCTGCGACAGAGCACTGAGATCTGGTCTTCCA 2132
Db      1980 CAAGGACTTGTGTGATGACACTACACAGCTGCGACAGAGCACTGAGATCTGGTCTTCCA 2039
Oy      2133 AAATGATATCATGAGATTATGACACCAAAATGTTTGGTATACAAACAAATGTAT 2192
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Db      2100 GAAATAGACATTTTGGATCTGGCACTGCGAGAGATATACAAATATGAGCATTTACAAAGAAC 2159
Oy      2253 CAGCAATGGAGCGGCTTCCAGCTACAGGAGATGCTGTCAACAAATATGAGCATTTACAAAGAAC 2312
Db      2160 CAGCAATGGAGCGGCTTCCAGCTACAGGAGATGCTGTCAACAAATATGAGCATTTACAAAGAAC 2219
Oy      2313 CAGCTATCAGAGATGATGCTGTGTCTTTCGGGGCTTAAATGAGGGAGATCTTCACTTAAG 2372
Db      2220 CAGCTATCAGAGATGATGCTGTGTCTTTCGGGGCTTAAATGAGGGAGATCTTCACTTAAG 2279

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Oy 430 GGCCGAGGGAGTGCCTAAGAGTGTGGCTGCTGTGAAGATGCGCGCTGATCAGTTGG 489
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Db 1915 AGAAATCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1974
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Db 2095 GGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2154
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Oy 2401 GAGAGACTTTTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460
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RESULT 4

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US-08-471-570-5
Sequence 5, application US/08471570
INVENTOR: US/08471570
GENERAL INFORMATION:
APPLICANT: IKARASHI, KOICHI
APPLICANT: SENOO, Masaharu
APPLICANT: MATANABE, Talsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: 18
ADDRESS: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
AIR: 02109
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471-570
FILING DATE: 06-JUN-1995
PRIORITY DATE: 05-SEP-1995
PRIORITY APPLICATION NO.: 05
PRIORITY APPLICATION DATE:
APPLICATION NUMBER: US/08/149,664
FILING DATE:
APPLICATION NUMBER: US 07/43369
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29822
REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
INFORMATION:
TELETYPE: 200291
STREET OR:
INFORMATION:
SEQUENCE CHAR. ID NO.: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURES:
NAME:
LOCATION:
US-08-471-570-5
Query Match 42.6%; Score 1817.2; DB 1; Length 1954;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1887; Consecutive 0; Mismatches 58; Indels 15; Gaps 2;
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1 GAGCGGGGATTGGTACCGTAAACCAATGCTGAGGCTCTTATCTGCTGCTGCTG 60
0Y 310 GTACACATGGACACTGTGCTGCTGCGCGGCGCTGCTGATGTTAGTTAGTAGATACACAC 369
DB 61 GTACACATGGACACTGTGCTGCTGCGCGGCGCTGCTGATGTTAGTTAGTAGATACACAC 120
0Y 370 TTATAGCGTCAAGAGAGCGACCAACCAATATCTCTCAACAGCAAGCTGTACGCGCT 429
DB 121 TTATAGCGTCAAGAGAGCGACCAACCAATATCTCTCAACAGCAAGCTGTACGCGCT 180
0Y 430 GCGCAGGAGAGTGCCTAGAGAGTGCCTGCTGCTGTTGAAGAGTCCGCGCTGATCAGTTGC 489
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0Y 490 AGCGAGGAGAGTGCCTAGAGAGTGCCTGCTGCTGTTGAAGAGTCCGCGCTGATCAGTTGC 549

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DB 241 ACTAAGATGGGTGATCGACTTGGGCGCCAAACATAGACAGTGTATTGGGGAGTACTTG 300
0Y 550 CACATTAAGGGGCGCCACGCCCTAGAGAGTCCGAGGCTCTATGCTGTATGCGCAGTAAAGCT 609
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0Y 670 CATGAGATGACACGATGTGCGAGAAATTTGTCTGTGAGAAACGTAAACAAAGAGA 729
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DB 849 AACCTGTCAAGTTTGTGCTGCCACGCGCGGAGAACCCATGCAACCATGCGGTGGCTG 600
0Y 850 AAAACCGGAGAGGTTTAAAGAGAGAGCGATGACAGGCTGACAGGTACAGAGTACAGAA 909
DB 601 AAAACCGGAGAGGTTTAAAGAGAGAGCGATGACAGGCTGACAGGTACAGAGTACAGAA 660
0Y 910 CACTGAGGCTCATATGAGAAAGTGTGTCATCTGACAGAGGAAATTAATCTGTGTG 969
DB 661 CACTGAGGCTCATATGAGAAAGTGTGTCATCTGACAGAGGAAATTAATCTGTGTG 720
0Y 970 GTGAGAAATGAAATAGGGGTCCATCATCACAGTACACAGCTGGAAGTTGTGTGAGCATG 1029
DB 721 GTGAGAAATGAAATAGGGGTCCATCATCACAGTACACAGCTGGAAGTTGTGTGAGCATG 780
0Y 1030 GTGAGGCGCCCATCTCTCAACCGGCAATCGCGCAATGCTCTCAACGAGTGTGAGAGA 1089
DB 781 CTTCAAGGCGCCCATCTCTCAACCGGCAATCGCGCAATGCTCTCAACGAGTGTGAGAGA 840
0Y 1090 GAGCTAAGATTGTGTGCAAGGTTTACAGTGAATGCCACGACCAACCTGAGATCAAG 1149
DB 841 GAGCTAAGATTGTGTGCAAGGTTTACAGTGAATGCCACGACCAACCTGAGATCAAG 900
0Y 1150 CAGGTGAAAGAGGCGTAAATTAATGCGGCGGAGCGGCGCTTACCTCAAGCTTCTC 1209
DB 901 CAGGTGAAAGAGGCGTAAATTAATGCGGCGGAGCGGCGCTTACCTCAAGCTTCTC 960
0Y 1210 AAGGCGCGCGGTGTAACACACGAGCAAGAAAGAAATGACGTCTCTAATATGGAATGA 1269
DB 961 AAGGCTGCGGAAATTAATGATTTCAATGAGAAAGGATGCTGTCTC -----AATGTC 1014
0Y 1270 AACTTTTGAAGAGCGTGGGGAATATAGCTGTGAGGAGGATATTCATTTAGTGTCTTT 1329
DB 1015 ACGGAGCGAGTGGGGGGAATATATATATATAGTCTTCATTAATATGCGAGCGAC 1074
0Y 1330 CACTGTCAATGTTGACAGTGTCTCC -----ACCGCTGGAAGAGAAAGAGGAT 1380
DB 1075 CACTGTCTCTGCGACGTCTCTCCAAACAGACACACCGCTGGAAGAGGAGAT 1134
0Y 1381 ACAGGATCTCCCAAGCTACAGAGAAATAGCACTTACATGATAGAGGCTCTTAAATGCC 1440
DB 1135 ACAGGATCTCCCAAGCTACAGAGAAATAGCACTTACATGATAGAGGCTCTTAAATGCC 1194
0Y 1441 TGTATGTGTATACAGTATCTCTGCGCAATGAGAAAGACAGCAAGAAAGCGAGACTTC 1500
DB 1501 TGTATGTGTATACAGTATCTCTGCGCAATGAGAAAGACAGCAAGAAAGCGAGACTTC 1254
0Y 1550 AGCAGCAGCGGCTGTGACAAAGCTGACAAAGAAATGAAATGAAATGAAAGCAAGCTTC 1580
DB 1255 AGCAGCAGCGGCTGTGACAAAGCTGACAAAGAAATGAAATGAAATGAAAGCAAGCTTC 1314
0Y 1561 GTTGTGCTGATGACAGTCTCTCATGAACTGCAACCGCGGTGAGTGAAGATTAACAA 1620
DB 1315 GTTGTGCTGATGACAGTCTCTCATGAACTGCAACCGCGGTGAGTGAAGATTAACAA 1374

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1621 CGCGCTCTTCACAGGACGACGACCCCGCTGCGAGGGGCTCCGAGATGAACTTCCA 1680
 1375 CGCGCTCTTCACAGGACGACGACCCCGCTGCGAGGGGCTCCGAGATGAACTTCCA 1434
 1681 GAGAGCCAAAATGGGAGTTTCGACAGATGACGACGAGCGGCGAGAGCCCTGGAGAA 1740
 1435 GAGAGCCAAAATGGGAGTTTCGACAGATGACGACGAGCGGCGAGAGCCCTGGAGAA 1494
 1741 GGTCTCTTTGGGCAAGTGTCTATGGGCGGAGCGAGGGAATTGACAAAGCAGCCCAAG 1800
 1495 GAGTCTCTTTGGGCAAGTGTCTATGGGCGGAGCGAGGGAATTGACAAAGCAGCCCAAG 1534
 1801 GAGTCTCTTTGGGCAAGTGTCTATGGGCGGAGCGAGGGAATTGACAAAGCAGCCCAAG 1860
 1555 GAGCGCTCTACCGCTGCGGCTGGAATGTTTAAAGATGATCCAGAGAAAGAACCTTTCT 1614
 1851 GATCTGGTGTACAGATGAGATGATGAAGATGATGGAAGAACAGAAATATCAATAAT 1920
 1615 GATCTGGTGTACAGATGAGATGATGAAGATGATGGAAGAACAGAAATATCAATAAT 1674
 1921 CTCTCTGAGCGCTGACACAGATGAGGCTGCTGATGATAGCTGATGATGATGATGAT 1980
 1675 CTCTCTGAGCGCTGACACAGATGAGGCTGCTGATGATAGCTGATGATGATGATGAT 1734
 1981 GCGAAGCTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
 1735 GCGAAGCTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1794
 2041 ATTACAGCTGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
 1795 ATTACAGCTGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1854
 2101 CTGCGCAGAGCATGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
 1855 CTGCGCAGAGCATGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1914
 2161 AGAATGCTTTGGTACAGAAACATGATGAGAAATG 2200
 1915 AGAATGCTTTGGTACAGAAACATGATGAGAAATG 1954
 RESULT 5
 US-08-471-570-9
 : Sequence 9, Application US/08471570
 : Patent No. 5750371
 : GENERAL INFORMATION:
 : APPLICANT: IGARASHI, KOICHI
 : APPLICANT: SENOO, Masaharu
 : APPLICANT: MATSUMBE, TATSUYA
 : APPLICANT: NAKAMURA, TOSHIKI. DNA AND USE THEREOF
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 : STREET: 130 Water Street
 : CITY: Boston
 : COUNTRY: Massachusetts
 : ZIP: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA
 : FILING DATE: 06-JUN-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/08/149, 664
 : FILING DATE: 05/07/733569
 : APPLICATION NUMBER: US 07/733569

FILING DATE: 16-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: LINER, Ernest V
 REGISTRATION NUMBER: 29822
 REFERENCE/DOCKET NUMBER: 40897
 TELEPHONE: (617)523-3400
 TELEFAX: (617)523-6440
 TELEX: 200291 STRE UR
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2310 base pairs
 TYPE: nucleic acid
 STRAND: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 25..1980
 US-08-471-570-9
 Query Match 39.7%; Score 1692.8; DB 1; Length 2310.
 Best Local Similarity 95.8%; Pval. No. 0;
 Matches 1778; Conservative 0; Mismatches 57; Indels 21; Gaps 3;

728 GAGCAGCCATACATGACACACACAAAGAGTGAAGAGGAGCTGACATGCTGTGCTGCGG 787
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 788 GCGACACTGTCAATTTGCTGCGCCAGCGCGGAGAGCCAAATGCAACATGCGGTGCG 847
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 848 TGAAGAACGAGAGATTAGACGAGGAGCTGCTGAGGCTGACAAAGTACGAAGAC 507
 254 TGAAGAACGAGAGATTAGACGAGGAGCTGCTGAGGCTGACAAAGTACGAAGAC 313
 908 AGCACTGAGAGCTCATATGAGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 967
 314 AGCACTGAGAGCTCATATGAGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 373
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 1148 AGCAGGTGAGAAAGAAAGCGCATTAATACGGGCGCGAGGGGCTGCTGCTGCTGCTGCTGCT 1207
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 1328 TTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1378
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Oy 1439 CTTGATGTTGGTACAGTCATCTCTGCGCAATGAGAAACAGACCAACGAGACACT 1498
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 Oy 1679 CAGACGACCCAAATGGAGATTTCACAGATTAAGCTGACACTGGGCAAGCCCTGGGAG 1738
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 Oy 1739 AAGCTTCTTTGGGAGAGTGTCTTCCGCGAGACAGTGGGAAATTAACAACCAACCCCA 1798
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 Oy 1799 AAGGACCCCTTACCTGGCTGTGAGATTTGAAGAATGATGCCACAGAGAAACACTTT 1858
 Db 1202 AAGGACCCCTTACCTGGCTGTGAGATTTGAAGAATGATGCCACAGAGAAACACTTT 1261
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 Db 1262 CTGATCTGGTGTCAAGATGAGATGATGAAGATGATGGCAACACAGAAATATCATAA 1321
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 Db 1322 ACTCTCTTGAGACCTGCGACACAGAGAGGCTCTCTTATGTCATAGTTGATGCTCTTA 1381
 Oy 1979 AAGGCAACCTCCAGAAATACCTTCGAGCCGAGACCCACCGGAGTGAAGTACCTCTATG 2038
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 Oy 2159 CCAAGGATCTTTGGTAAAGCAAAACATGCAAAATGCAAAATGCAAAATGCAAAATG 2218
 Db 1562 CCAAGGATCTTTGGTAAAGCAAAACATGCAAAATGCAAAATGCAAAATGCAAAATG 1621
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 Oy 2279 GAGATGCTCGAAGAGCCCTGTTGATTAAGATPACATCATCAAGAGATGATCTGCTCC 2338
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 Db 1742 TCGAGGTGTTAATGTGAGATCTTCACTTTAGGAGGCTCCGCCCTACCAAGCAAGTCCCG 1801
 Oy 2399 TCGAGGTGTTAATGTGAGATCTTCACTTTAGGAGGCTCCGCCCTACCAAGCAAGTCCCG 2458
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 Oy 2459 CCAAGCACTGTACATGATGATGAGGACTGTGTGCAATGCAAGTGCCTCCCGAGACCA 2518
 Db 1862 CCAAGCACTGTACATGATGATGAGGACTGTGTGCAATGCAAGTGCCTCCCGAGACCA 1921
 Oy 2519 CTTCAAGCAGCTTGTGTAAGACTTGTGATGCAATTCACCTTCACACCAAGTGAAG 2574

Db 1922 CTTCAAGCAGCTTGTGTAAGACTTGTGATGCAATTCACCTTCACACCAAGTGAAG 1977
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 US-08-070-165F-5
 ? Sequence 5, Application US/08070165F
 ? Patent No. 5750365
 ? GENERAL INFORMATION:
 ? APPLICANT: Chiu, Ing-Ming
 ? APPLICANT: Poulin, Matthew L
 ? TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
 ? NUMBER OF INVENTION: 12
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESS: Ing-Ming Chiu
 ? STREET: 52052 Davis Medical Research Center, 480 West
 ? STREET: 9th Avenue
 ? CITY: Columbus
 ? STATE: Ohio
 ? ZIP: 43210 USA
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patentin Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? FILING DATE: 05/08/07.0, 165F
 ? CLASSIFICATION: 435
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (614)-293-8093
 ? TELEFAX: (614)-293-5631
 ? INFORMATION FOR SBO ID NO.: 5:
 ? SBO ID NO.: 5
 ? SBO LENGTH: 2675 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: double
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: cDNA
 ? HYPOTHETICAL: NO
 ? NITE SENSE: NO
 ? NITE ANTISENSE: NO
 ? ORIGIN: SBO
 ? ORGANISM: No. 5750365ophthalmus viridescens
 ? DEVELOPMENTAL STAGE: Adult
 ? TISSUE TYPE: Regenerating forelimb blastema
 ? CELL TYPE: Mesenchyme and Epithelium
 ? IMMEDIATE SOURCE:
 ? LIBRARY: lambda gcl1
 ? CLONING VECTOR: lambda
 ? POSITION: 14725
 ? POSITIVE: YES
 ? UNITS: bp
 ? FEATURE:
 ? NAME/KEY: 5'UTR
 ? LOCATION: 1..324
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: 325..2511
 ? FEATURE:
 ? NAME/KEY: 3'UTR
 ? LOCATION: 2512..2675
 ? PUBLICATION INFORMATION:
 ? AUTHORS: Poulin, Matthew L
 ? TITLE: Nucleotide sequences of two new
 ? TITLE: (No. 5750365)ophthalmus viridescens) fibroblast growth
 ? JOURNAL: Biochim. Biophys. Acta
 ? VOLUME: 1220
 ? PAGES: 209-211
 ? DATE: 1994
 ? RELEVANT RESIDUES IN SBO ID NO.: 5: FROM 1 TO 2675
 ? US-08-070-165F-5

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Query Match          32.0%; Score 1367.6; DB 1; Length 2675;
Best Local Similarity 79.1%; Pred. No. 0;
Matches 1694; Conservative 0; Mismatches 429; Indels 9; Gaps 2;

Oy 648 AGATGCAATCTATCCCGGAGATGATGAGACAGCAACAGCGGCTGGAGATTTCACAA 491
Db 432 AGATGCAATCTATCCCGGAGATGATGAGACAGCAACAGCGGCTGGAGATTTCACAA 491

Oy 708 TGGAGACAGTACACAAAGAGACAGCATATCGACCAACAGAAAGATGAGAAACCC 767
Db 492 TGGACAC--AACCAACATAGAGGCTCCCTATCGACCAATACAGAAATGAGAAACAA 548

Oy 768 GGTCTATGCTGCTGCTGCGCAACAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 827
Db 549 ACTCATGCTGCTGCTGCTGCGCAACAGCTGATGCTGCTGCTGCTGCTGCTGCTG 608

Oy 828 AATGCAACATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 887
Db 609 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666

Oy 886 AAGGCTAAGGTACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAAC 947
Db 669 TGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 666

Oy 869 CGGCTTAAAGGTACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAAC 728
Db 669 CGGCTTAAAGGTACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAAC 728

Oy 948 CAGGGAATATATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1007
Db 729 CGAGGCAACATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 788

Oy 1008 CTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1067
Db 789 CTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 848

Oy 1068 TGGCTCACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1127
Db 849 CAGACACACAAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 908

Oy 1128 GCGCCACATCCAGTGCATACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAAC 1187
Db 909 GCGCAATATCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 968

Oy 1188 GCTGCTCTACTGCAAGGCTTCCAGGCGCGCGGTGTAAACACAGCAACAAAGATTGA 1247
Db 969 GCAATCCATCTGCAAGGCTTCCAGGCGCGCGGTGTAAACACAGCAACAAAGATTGA 1028

Oy 1248 GGTCTCTATATTCGGAATGTAATCTTTTGAGAGACGCTGGGAATATATACGCTTGG 1307
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Db 1089 TAAATCTATGGAATATCTTCACTGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 1148

Oy 1368 AGAAAGAGATTAACAGCTTCCCAAGCTACGTGAAATACGCTTATTCGATGCAAGAG 1427
Db 1149 GGAAGCTGAG----TTTCATCATGGAAGTATTCGAAATATTCGATGCAAGAGAG 1202

Oy 1428 CTCTTAAATTCGCTGATATGCTGCTGCAAGCAATCTGCTGCTGCTGCTGCTGCTGCTG 1487
Db 1203 CTCTTCAATCACTGATATGCTGCTGCAAGCAATCTGCTGCTGCTGCTGCTGCTGCTG 1262

Oy 1488 GAAGCGAGACTTACAGAGCGCGCTGCTGCAACAGCAACAGCAACAGCAACAGCAAC 1547
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Oy 1548 GAAGCGAGACTTACAGAGCGCGCTGCTGCAACAGCAACAGCAACAGCAACAGCAAC 1607
Db 1343 CAGAGAGATTAACAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1382

Oy 1608 GAGGATTAACACAGCGCTCTGCTGCAACAGCAACAGCAACAGCAACAGCAACAGCAAC 1667
Db 1383 CGAGATTAACACAGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1442

Oy 1668 GTATGAACTTCCAGAGAGCAACAAATGGAAGTTTCCAGAGATTAACGTGACATCGG 1727

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Db 1443 GTATGAACTTCCAGAGAGCAACAAATGGAAGTTTCCAGAGATTAACGTGACATCGG 1502
Oy 1728 GCCCTGCGAGAAAGGTGCTTTTGGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1787
Db 1503 GCGCTGCGAGAGAGCTTCTTGGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1562
Oy 1788 AAGCAACCCCAAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1847
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Oy 1848 GAAAGACTTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1907
Db 1623 GAAAGACTTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1682
Oy 1908 GAATATCATTAATCTTGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1967
Db 1683 AATATATCATTAATCTTGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1742
Oy 1968 GTATGCTTAAAGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2027
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Oy 2028 GTATGCTTAAAGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2087
Db 1803 GTATGCTTAAAGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1862
Oy 2088 ATGCACTGCAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2147
Db 1863 TTGCAAGTACCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1922
Oy 2148 AGATTTAGCAGCAAGATGTTTGGTAAAGCAACAAATGATGCAAAATGACAGACTT 2207
Db 1923 GCACTTGGCAGCTGCAAGATGTTTGGTAAAGCAACAAATGATGCAAAATGACAGATT 1982
Oy 2208 TGGCACTGCGAGATGATGCAATATGATGCAATATGCAAAAGCAACAGCAATGCTGCTG 2267
Db 1983 TGGTTTGGCAGCAAGATGATGCAATATGATGCAATATGCAAAAGCAACAGCAATGCTGCTG 2042
Oy 2268 TGCAGTAAATGATGCTGCTGCAAGAGCCCTGTTTGAATGAGATATTCATCATGAGCTG 2327
Db 2043 CCGCTGCAAGTGAATGCTGCTGCAAGAGCCCTGTTTGAATGAGATATTCATCATGAGCTG 2102
Oy 2328 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2387
Db 2103 CGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2162
Oy 2388 AGGATATCTCTGAGAGAACTTTTAACTGCTGAGAGAGCAACAGCAATGATGATTAACC 2447
Db 2163 TGGATTTTCACTGATGAGAACTTTTAACTGCTGAGAGAGCAACAGCAATGATGATTAACC 2222
Oy 2448 AGCAATGCAACAGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2507
Db 2223 TGGCAATGCAACAGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2282
Oy 2508 CCAAGAGCAAGCTTCAAGCAAGCTTGGTGAAGAGCTGATGATGATGATGATGATGATG 2567
Db 2283 CCAAGAGCAAGCTTCAAGCAAGCTTGGTGAAGAGCTGATGATGATGATGATGATGATG 2342
Oy 2568 CAGTGAAGATTAATGCAAGCTTCAAGCAAGCTTGGTGAAGAGCTGATGATGATGATGATG 2627
Db 2343 CAGTGAAGATTAATGCAAGCTTCAAGCAAGCTTGGTGAAGAGCTGATGATGATGATGATG 2402
Oy 2628 CAGCAAGATCTTCTGTTTCTGCAAGATGATGATGATGATGATGATGATGATGATGATG 2687
Db 2403 TACAGAGATTTCTGCTTCTGCAAGATGATGATGATGATGATGATGATGATGATGATG 2462
Oy 2688 CGAGCACTGCTCTGCTGATGCAATGATGATGATGATGATGATGATGATGATGATGATG 2739
Db 2463 CGAGCCTCTGCTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 2514

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RESULT 7

QY 2159 CCGAAGATGTTTGGTAACGAAGAACAATGTGCTAAATTG 2200
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 Db 1562 CCGAAGATGTTTGGTAACGAAGAACAATGTGCTAAATTG 1603
 RESULT 9
 US-08-070-165F-9
 : Sequence No. Application US/08070165F
 : Patent No. 5750365
 : GENERAL INFORMATION:
 APPLICANT: Chiu, Ing-Ming
 APPLICANT: Poulin, Matthew L.
 ATTORNEYS: American Academic Fibroblast Growth Factor (ARCF)
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ing-Ming Chiu
 STREET: 52052 Davis Medical Research Center, 480 West
 STREET: 9th Avenue
 CITY: Columbus
 STATE: Ohio
 COUNTRY: USA
 ZIP: 43210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 05/08/07,0.165F
 CLASSIFICATION: A35
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (614)-293-8093
 TELEFAX: (614)-293-5631
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 486 base pairs
 TYPE: nucleotide
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: SV57036Sophilthalmus viridescens
 DEVELOPMENT STAGE: embryo
 TISSUE TYPE: Regenerating forelimb blastema
 CELL TYPE: Mesenchyme and Epithelium
 IMMEDIATE SOURCE:
 LIBRARY: lambda gt11
 CLONE: Kp19-1
 POSITION IN GENOME:
 FEATURE:
 NAME/KEY: bp
 NAME/KEY: 5'UTR
 LOCATION: 1..324
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 325..2517
 FEATURE:
 NAME/KEY: 3'UTR
 LOCATION: 2518..2681
 PUBLICATION INFORMATION:
 AUTHORS: Poulin, Matthew L
 TITLE: Nucleotide sequences of two new
 TITLE: (no. 575036)Sophilthalmus viridescens) fibroblast growth factor
 TITLE: factor receptor-2 variants
 VOLUME: 1220
 PAGES: 209-211
 DATE: 1994
 RETRIEVAL RESIDUES IN SEQ ID NO: 9: FROM 1 TO 2681

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US-08-070-1.65E-9
Query Match      29.9% Score 1276.4: DB 1: Length 2681:
Best Local Similarity 26.6%: Field No. 8-66-704:
Matches 1007: Conservative 0: Mismatches 476: Indels 15: Gaps 3:

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Db 432 AATGTGCAAACTCATGAGGATGATGAAGACAAACACGCGTCGTGATTCACAA 491
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 708 TGACAAACAGTACAAACAGACAGACACATCTGACACAAACAGAACATGAAAAAGC 767
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Db 492 TGACAAAC---ACCAACATGAGGCTCCGTATCTGAGAAATACAAATATGAAAAAGAA 548
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RESULT 10
 US-08-885-418-9
 Sequence 9: Application US/0885418
 Patent No. 5925528
 GENERAL INFORMATION:
 APPLICANT: Chiu, Ing-Ming L
 APPLICANT: Poulin, Matthew L
 TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aGFG)
 NUMBER OF SEQUENCES: 12
 COMPLETION ADDRESS: Chiu
 STREET: 52052 Davis Medical Research Center, 480 West
 STREET: 9th Avenue
 CITY: Columbus
 STATE: Ohio
 COUNTRY: USA
 ZIP: 43210
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: PC-DOS/MS-DOS
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/885,418
 CLASSIFICATION: 435
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (614)-293-8093
 TELEFAX: (614)-293-5631
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2681 base pairs
 STRANDEDNESS: double
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGIN: SOURCE: 5925528opththalmus viridescens
 ORGANISM: HUMAN
 TISSUE TYPE: Regenerating forelimb blastema
 CELL TYPE: Mesenchyme and Epithelium
 IMMEDIATE SOURCE:
 LIBRARY: lambda gt11
 CLONE: KP19-1
 POSITION IN GENOME:
 FEATURES:
 NAME/KEY: 5' UTR
 LOCATION: 1..324
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 325..2517
 FEATURE:
 NAME/KEY: 3' UTR
 LOCATION: 2518..2681
 PUBLICATION INFORMATION:
 AUTHORS: Poulin, Matthew L
 TITLE: Nucleotide sequences of two new
 TITLE: (No. 5925528opththalmus viridescens) fibroblast growth
 TITLE: factor receptor-2 variants
 JOURNAL: J Biol Chem, Biophys, Acta
 VOLUME: 1220
 PAGES: 209-211
 DATE: 1994
 RELEVANT RESIDUES IN SEQ ID NO: 9: FROM 1 TO 2681
 US-08-885-418-9
 Query Match 29.9%, Score 1276.4, DB 2, Length 2681:
 Best Local Similarity 76.8%, Field. No. 8,6e-304,

Matches 1607: Conservative 0: Mismatches 476: Indels 15: Gaps 3:
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 Oy 1823 AGATGTTGAAGATATGCTGCAAGAAAGCAAGCTTGTGATCTGGTGTCAAGATGGA 1882
 Db 1541 AGATGTTGAAGATATGCTGCAAGAAAGCAAGCTTGTGATCTGGTGTCAAGATGGA 1600

Oy 1883 TGATCAGATGATTTGGAAACAAAGAAATATCTAATCTTGGAGGCTGCACAGG 1942
 Db 1601 TGATCAGATGATTTGGAAACAAAGAAATATCTAATCTTGGAGGCTGCACAGG 1660
 Oy 1943 ATGGCCCTCTCTATCTATGATGATATGCTCTTAAAGGCAAGCTGCGAGATACCTCC 2002
 Db 1661 ATGGCCCTCTCTATCTATGATGATATGCTCTTAAAGGCAAGCTGCGAGATACCTCC 1720
 Oy 2003 GAGCCCGAGAGCCACCGGGATGAGATACCTCTAAAGCAAGCTGCTGAGAGG 2062
 Db 1721 AGGCCCGAGAGCCCGGGATGAGATACCTCTAAAGCAAGCTGCTGAGAGG 1780
 Oy 2063 AGATACCTTCAAGCACTGTGGTGAATGCTGACAGCAAGCTGCGAGAGATGAGATCT 2122
 Db 1781 AGCTCTCTCCAGAGGACTGGTGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1840
 Oy 2123 TGGCTTCCCAAAATGATATGATGATGATTAAGCAAGCAAGCAAGCAAGCAAGCAAG 2182
 Db 1841 TGGCTTCCCAAAATGATATGATGATGATTAAGCAAGCAAGCAAGCAAGCAAGCAAG 1900
 Oy 2183 ATAGTGTGATGAATATAGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 2242
 Db 1901 ACAATGTGATGATGATATAGCAAGATGATGATGATGATGATGATGATGATGATGAT 1960
 Oy 2243 ACAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2302
 Db 1961 ATAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2020
 Oy 2303 ATAGAGATATAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2362
 Db 2021 ACCGATATCAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2080
 Oy 2363 TCACTTAAAGGAGGCTGCGCTTACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2422
 Db 2081 TCACTTAAAGGAGGCTGCGCTTACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2140
 Oy 2423 AGAAGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2482
 Db 2141 AGAAGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2200
 Oy 2483 GGAAGTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2542
 Db 2201 GGAAGTGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2260
 Oy 2543 TGAATCAATCTCACTCTGCAACCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2602
 Db 2261 TGAATCAATCTCACTCTGCAACCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2320
 Oy 2603 AACATATCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2659
 Db 2321 AACATATCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 2380
 Oy 2659 CTGATTTTCTGCAAGCCCATCTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2712
 Db 2381 CGGTCTCTCTCATATGAGCCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2433

RESULT 12
 US-08-459-296-1
 ? Sequence 1. Application US/08459296
 ? Patent No. 5670323
 ? GENERAL INFORMATION:
 ? APPLICANT: No. 5670323, Michael
 ? APPLICANT: Gonzalez, Ana-Maria
 ? APPLICANT: Gonzalez, Ana-Maria
 ? TITLE OF INVENTION: PROCESS FOR DETECTION OF NEUROPLASTIC
 ? TITLE OF INVENTION: PROCESS FOR DETECTION OF NEUROPLASTIC
 ? NUMBER OF SEQUENCES: 2
 ? CORRESPONDENCE ADDRESSES:
 ? ADDRESS: Pennie & Edmonds
 ? STREET: 1195 Avenue of the Americas
 ? CITY: New York
 ? STATE: NY

Db 1761 ACCTCTCTCCAGAGACCTGGTCTCTGCGCTTACCGAGGTGGCCGAGAGCATGAGATTC 1840
 Oy 2123 TGGCTTCCAAAAATGATATCTGAGATTTAGCAGCCGAGAAATGCTTTGGTATACGAA 2182
 Db 1841 TGGCTTCCAAAAATGATATCTGAGATTTAGCAGCCGAGAAATGCTTTGGTATACGAG 1900
 Oy 2183 ACATATGATGATATATACGAGACTTGGATCGGACAGAGATATACAAATATATAGATATT 2242
 Db 1901 ACATATGATGATATATACGAGACTTGGATCGGATCGGAGAGATATACAAATATATAG 1960
 Oy 2243 ACAAAAAGCAGCAATGGGGGGCTTACATGAGAGATGATGGTGTGCAAGGCTTTGTC 2302
 Db 1961 AAAAAAGCAGCAATGGGGGGCTTACATGAGATGATGGGATGGGACCGAGGATTATTT 2020
 Oy 2303 ATATAGATATAGATCATGAGATGATATGCTGGGTGGGTATTAAGTGGGAAATATC 2362
 Db 2021 ACCGATATAGACACCCAGAGAGATGATGATGCTGGGGGATGATTAAGTGGGAAATATC 2080
 Oy 2363 TCACTATAGAGGGGGCTTCCCTTACCGAGAGATGATGCTGGGGGATGATTAAGTGGG 2422
 Db 2081 TCACTATAGAGGGGGCTTCCCTTACCGAGAGATGATGCTGGGGGATGATTAAGTGGG 2140
 Oy 2423 AGCAAGGACACAGATATGATTAAGCGAGCAATGATGATGATGATGATGATGATGATG 2482
 Db 2141 AGCAAGGATACCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2200
 Oy 2483 GGGATCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2542
 Db 2201 GGGATCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2260
 Oy 2543 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2602
 Db 2261 TGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2320
 Oy 2603 AACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2659
 Db 2321 AACGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2380
 Oy 2660 CTGTTTTTCTCCAGACCCATGCTTACGACACATGATGATGATGATGATGATGATGATG 2712
 Db 2381 CGCTCTCTCTCATGAGCCGCTGCGAGAGACCTGCTCCGCCGACACCA 2433

RESULT 13
 US-07-997-133-2
 Sequence 2, Application US/07997133
 GENERAL INFORMATION:
 APPLICANT: Bergonzoni, Laura
 APPLICANT: Bergonzoni, Laura
 APPLICANT: Isaacchi, Antiochia
 APPLICANT: Roncucci, Romeo
 APPLICANT: Samiencos, Paolo
 TITLE OF INVENTION: Extracellular Form of the human
 TITLE OF INVENTION: Fibroblast Growth Factor Receptor
 NUMBER OF SEQUENCES: 8
 COMPLETION ADDRESS:
 ADDRESS: P. C. STRIYAK, MCCLELLAND, MAIER & NEUBAUER,
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 ZIP: 22202
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/997,133
 FILING DATE: 28-DEC-1992
 PRIORITY DATE: 28-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/642,755

? FILING DATE: 18-JAN-1991
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BOLDON, Norman F.
 ? PHONE: 800-368-7454
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (703)521-4500
 ? TELEFAX: (703)486-2347
 ? TELEX: 248855 OPAT UR
 ? INFORMATION FOR SEQ ID NO: 2:
 ? SEQUENCE CHARACTERISTICS:
 ? TYPE: nucleic acid
 ? STRANDEDNESS: unknown
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? US-07-997-133-2
 ?
 ?
 Query Match 27.7% Score 1182.2 DB 5: Length 2469:
 Matches 1616: Conservative 0: Mismatches 653: Indels 24: Gaps 3:
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 Oy 458 GCGTGTGAAAGATCCGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 517
 Db 167 GGTGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 226
 Oy 518 ACATATAGACAGTGTATTTGAGAGATCTTGGAGATTAAGAGCCGACGCTAGAGACT 577
 Db 227 GCACCCGACCCCATCATCAGGGGAGAGGTGAGAGTGGAGACTCCGTGCGCAGACT 286
 Oy 578 CGGCGCTATGCTGTACTGATGCGAGTAGGAGCTGTAGACAGTGAACCTTGTACTGATG 637
 Db 287 GCGGCTATGATGCTGTACTGATGCGAGTAGGAGCTGTAGACAGTGAACCTTGTACTGATG 346
 Oy 638 TGAATGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 697
 Db 347 TCAATGTTTCAATGCTGCTCCCTGCGAGAGATGATGATGATGATGATGATGATGATGATG 406
 Oy 698 ATTTGTGATGAGAAAGATTAACACAA-----GAGACACCATATCTGCA 742
 Db 407 CAGAGAGAAAGAAAGATTAACACAAACCAACGATATGCGGTATGCTATATTGCA 466
 Oy 743 GCACACAGAAAGAAAGATTAACACAAACCAACGATATGCGGTATGCTATATTGCA 802
 Db 467 CATTCCGAGAAAGATTAACACAAACCAACGATATGCGGTATGCTATATTGCA 526
 Oy 803 TTTCGTTGCCAGCCGGGAGACCAATGACCAACCATGCGGTGGTGAAGAAAGGGAGAG 862
 Db 527 TCAATATGCTTCCAGTGAAGAGACCAACCCACACCTGCGGTGTTGAAATATGACAA 586
 Oy 863 AGTAAAG 922
 Db 587 AATTCAAACCTACACAGAGATTAAGAGGCTTACAGAGTCCGTATGCCACTGAGAGACT 646
 Oy 923 TTATGAAAGTGTGCTCCATGTAAAGAGGAATATATCTGTGTGTGGAGAAATTA 982
 Db 647 TATAGACTGTGTGTGCTCCATGTAAAGAGGAATATATCTGTGTGTGGAGAAATTA 706
 Oy 983 AGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1042
 Db 707 AGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 766
 Oy 1043 TCTCTCAACCCGATGCTGCGAGAAATGCTTCCACAGATGATGATGATGATGATGATGATG 1102
 Db 767 TCTCTCAACCCGATGCTGCGAGAAATGCTTCCACAGATGATGATGATGATGATGATGATG 826
 Oy 1103 TCTCTCAACCCGATGCTGCGAGAAATGCTTCCACAGATGATGATGATGATGATGATGATG 1162
 Db 827 TGTGTAAGCTGTACAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 886
 Oy 1163 AGCGAGTAAATACAG 1222
 Db 887 ATGGAGACAAATGAG 946

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1233 TTAACACAGGACAAAGAGATTAGCTTCTATTATGCGAATGTAACTTTGAGAGAC 1282
1234 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
947 TTTATACACAGGACAAAGAGATTAGCTTCTATTATGCGAATGTAACTTTGAGAGAC 1306
1283 CTGGGGAATATAGCTGCTGGGGAATATATGAGGATATCTTCACTGCTGGAGTGT 1342
1284 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
1007 CAGGGAGATATAGCTGCTGGGGAATATATGAGGATATCTTCACTGCTGGAGTGT 1066
1343 TGCAGGTTCTGCAGGCTGTGGAGAGAAAGAGAAATTAACGCTTCCCGAGCTACCTGG 1402
1067 TGCAGGTTCTGCAGGCTGTGGAGAGAAAGAGAAATTAACGCTTCCCGAGCTACCTGG 1126
1403 AGATGACATTTATCTGCAATAGGAGCTCTCTTAATGAGCTGATGCTGCTGATACCTAG 1482
1127 AGATGACATTTATCTGCAATAGGAGCTCTCTTAATGAGCTGATGCTGCTGATACCTAG 1186
1463 TGTGCGCAATCAGAAACAGACAGAACAGACCACTTACAGACCCGCGCTGTGCACA 1522
1167 TCTTAAAGATGAGAAAGCTGTACACAAAGAGATGCTTCCACACCAAGATGCTGTGCTCA 1246
1523 AGCTGACCAAAAGCTTATCCCGCTGGGAGAAAGATGATACATTTGGCTGAGTGCAGCTGT 1582
1247 AGCTGACCAAAAGCTTATCCCGCTGGGAGAAAGATGATACATTTGGCTGAGTGCAGCTGT 1306
1563 CAGTGAACCTCCAAACCGCGCTGGTAGATTAACAAACAGCCTCTCTTCACAAACGACAGCA 1642
1307 CAGTGAACCTCCCGGCTCTCTTCTGATTCGGGCAATACAGGCTC-----TCTCTCAAGTGTGCA 1360
1643 CCGCCATGCTGGAGAGGCTCTCCGATGTACACTTCCAGAGAGACCCAAATGGGAGATTTC 1702
1361 CTCCCATGCTAGCAAGGCTCTCTTCACTTACGCTTCCGAGAGACCTCTGGAGAGCTGTG 1420
1703 CAGAGATTAACCTGACACTGGGCAACCCCTGGAGAGAGCTTCTTGGGCAAGTGTCTCA 1762
1421 CTGGGAGAGAGCTGCTTATAGCAAAACCTCGTGAAGAGGCTCTTGGAGAGTGTGCT 1480
1763 TGGGAGAGAGCTGAGGAAATTTGAAAGAGACAAACCCAAAGAGAGGCTGACAGCTGGCCCTGCA 1822
1481 TGGGAGAGAGCTGAGGAGGCTGAGCAAGAAACCCAAAGAGAGGCTGACAGCTGGCCCTGCA 1540
1823 AGAGATTGAAGATTAACGCAACAGAAAGAAACCTTTGATCTGCTGTCAAGAGTGCAGA 1882
1541 AGAGATTGAAGTGGAGAGCAACAGAAAGAAATTTGTGATGATCTGTCAAGAAATGCAGA 1600
1883 TGTATGAAGATGATTGGAGAAACAAATATGATTAATCTTGTGAGACCTGACACAGG 1942
1601 TGTATGAAGATGATTGGAGAGCAATTAAGATTAATGATTAATCTTGTGAGACCTGACACAGG 1660
1943 ATGGGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2002
1661 ATGGGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1720
2003 GAGGCCGAGAGCCAGCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2062
1721 GAGGCCGAGAGCCAGCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1780
2063 AGAGGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2122
1781 AGGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1840
2123 TGGCTTCCCAAAATATCTTATCATGATGATGATGATGATGATGATGATGATGATGATGATG 2182
1841 TGGCTTCCCAAAATATCTTATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1900
2183 AGAGGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2242
1901 AGAGGCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1960
2243 ACAGAAAGACACCAATGAGGAGCTTCCATCATGATGATGATGATGATGATGATGATGATGATG 2302
1961 ATTAAGAAAGACCAATGAGGAGCTTCCATCATGATGATGATGATGATGATGATGATGATGATG 2020

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2303 ATGAGATTAACACTATCATGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 2362
2021 ACCGATATACACCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2080
2363 TCACTTTAGGGGGCTCTGCGCTACCAAGAGATTTCCCTGGAGACACTTTTAAGCTGTCA 2420
2081 TCACTTTAGGGGGCTCTGCGCTACCAAGAGATTTCCCTGGAGAGACTTTTAAGCTGTCA 2140
2423 AGAAGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2482
2143 AGAAGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2200
2483 GGGAGGTTTGGCAATGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2542
2201 GGGAGGTTTGGCAATGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2260
2543 TGGATCAATTTCTGACTTCACACGATTAAGAGAAATTAAGAGAGAGAGAGAGAGAGAGAG 2602
2261 TGGAGCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2320
2603 AGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2659
2321 ACCAGTATCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2380
2660 CTGTTTCTTCTGCAACACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2712
2381 CGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2433

RESULT 14
US-08-451-822A-14
Sequence 14, Application us/08451822A
Patent No. 5863888
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
INVENTOR: Dionne, Craig A
APPLICANT: Jaffe, Michael C
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: 100 Rhone-Poulenc Rorer Legal Department
CITY: Collegenville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPILED BY: IBM PC COMPATIBLE
SOFTWARE: SYMBIOSIS/MS-DOS
CURRENT APPLICATION DATA:
Filing Date: 08/451.822A
CLASSIFICATION: 435
PRIORITY INFORMATION:
PRIORITY INFORMATION: US 08/323,430
PRIORITY INFORMATION: 1394
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIORITY INFORMATION:
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A0496E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR SBO ID NO: 14:

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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 2662 base pairs
;     TYPE: nucleotide
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     US-08-451-822A-14

Query Match      27.7%  Score 1180.6  DB 2:  Length 2662:
Sequence Similarity 27.8%  Pident No. 2,396-280:
Matches 1631:  Conservative  0;  Mismatches 644;  Indels  24;  Gaps  3;

Oy  458  GCCTCTGGAAAGATGCGCCGCTGATCAATGGTGAAGATGAGACCTTGGGGGCCCA 517
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  254  GCGTCGGGAGACGATGCGAGACACTACTGCTCGGGAGCGGGGTCAGCTGGCGGAA 313
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  518  ACAGTAAAGACAGTGGCTATTATGGGCAATCTTGGAGATTAAGGGCCGACGGCTAGAG 577
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  314  GCACCCGACCCGCAATCAGAGGGAGAGATGAGATGAGATGAGATGAGATGAGATGAG 373
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  578  CCGGCGCTATGCTGTATCTGACGAGAGAGAGTGAAGACCTTGGTATGGTATGGTAT 637
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  374  CGGCGCTATGCTGTATGCTGTATGACAGACCCCTGGGGGACAGTGAACCCCTTCTCG 433
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  638  TGAATGTCAAGATAGTGCATCTGATCCGGAATGATGATGATGATGATGATGATGATG 697
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  434  TCATGTCTTCAGATGCTCTCTCCCTCGAGGATGATGATGATGATGATGATGATGATG 493
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  658  ATTGTGTCAAGTGAAGAGTAAACACA-----GAGAGACCAATAGCTGA 742
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  494  CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 553
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  743  CGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 802
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  554  CATTCCCAAGAAAGATGAGAAAGAAATTGCGATGCGAGTCCCGGCTCCAGAGATGA 613
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  803  TTGCGTCCCAAGCCGAGGGAGACCAATGCGCAACATGCGGTGGGTGAGAAAGAG 862
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  614  TCGAATGCGCTTCAATGAGAGACCCCAACCCGACCTGCGGTGTTGAAAAATGGCAAG 673
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  863  AGTTTAAAGAGAGATGCGATGAGAGAGTACAGAGTACAGAGAGAGAGAGAGAG 922
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  674  AATTCAACCTGACACAGAGATGAGAGCTGACAGAGCTGTTATGCCACTGGACATCA 733
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  923  TTATGGAAGATGTGTCCCATCTGTACAGAGGAAATTAATCTGTGTGGTGAATGAAT 982
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  734  TATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 793
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  983  ACGGGTCCATCATCAGAGTACCACTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1042
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  794  ACGGAGCATCAACAGACATACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 853
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
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Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  854  TCTCTCAAGCCGATCTGCGGCAATGCTCTGCTCAAGTGTGTGTGTGTGTGTGTGTGT 913
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  1103  TCTGCAAGGTTTACAGTGTATGCCACCCCACTCACTGAGTGAATCAACAGTGAAGA 1162
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  914  TGTGTGAGGTGTACAGTGTACCCGACCCGACATTCAGTGGCTAAACAGTGAAGTGA 973
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  1163  ACGCGATTAATACAGGCGCCGAGGCTGCTCTCAAGTGTGTGTGTGTGTGTGTGTGT 1222
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  974  ATGCGAGCAATGTGGCCAGACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1033
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  1223  TTATCAACACAGGAGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1282
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  1034  TTATATACACAGGAGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1093
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  1283  CTGGGAGATATACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1342
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  1094  CAGGGAGATATACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1153
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |
Oy  1343  TGACGATCTGACAGCGCTGAGAGAGAAAGAGATACAGCTTCCCAAGTACTGTG 1402
Db    | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 |

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Db  1154  TGACGATCTGACAGCGCTGAGAGAGAGAGAGAGAGATACAGCTTCCCGCTGACTGTG 1213
Oy  1403  AGTATAGCAATTTACTGTACAGAGGCTCTTTATATGCGCTGTATGTGTGTGTGTGTGT 1462
Db  1214  AGATCATCATTTATTTGTCAAGAGGGGCTTCTCTATCTGTGTGTGTGTGTGTGTGTGT 1273
Oy  1463  TGTGCCAATATGAAGACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1522
Db  1274  TGTCAAGATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1333
Oy  1523  TGTCAAGATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1582
Db  1334  AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1393
Oy  1583  CAGTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1642
Db  1394  CAGTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1447
Oy  1643  CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1702
Db  1448  CTTCCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1507
Oy  1703  CAAGAGATTAAGCTGACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1762
Db  1508  CTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1567
Oy  1763  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1822
Db  1568  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1627
Oy  1823  AGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1882
Db  1628  AGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1687
Oy  1883  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1942
Db  1688  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747
Oy  1943  ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2002
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Oy  2003  GAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2062
Db  1808  AGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1867
Oy  2063  AGTATAGCAATTTACTGTACAGAGGCTCTTTATATGCGCTGTATGTGTGTGTGTGTGT 2122
Db  1868  AGTATAGCAATTTACTGTACAGAGGCTCTTTATATGCGCTGTATGTGTGTGTGTGTGT 1927
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Db  1928  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1987
Oy  2183  ACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2242
Db  1988  ACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2047
Oy  2243  ACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2302
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Db  2108  ACCGATATATATATATATATATATATATATATATATATATATATATATATATATATAT 2167
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 Db 2528 TTGCAATC 2536
 RESULT 15
 US-08-323-430-14
 ; Sequence 14: Application US/08323430
 ; Patent No. 5344316
 ; TITLE: INFORMATION:
 ; APPLICANT: Dione, Craig A
 ; APPLICANT: Crumley, Greg
 ; APPLICANT: Jey, Michael C
 ; APPLICANT: Schlusser, Joseph
 ; TITLE OF INVENTION: Fibrinolytic Growth Factor Receptors
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER ADDRESS:
 ; ADDRESS: 500 Arcola Road
 ; STREET:
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER AVAILABLE FROM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/323.430
 ; FILING DATE: 06/08/93
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US to be assigned
 ; FILING DATE: 21-AUG-1992
 ; APPLICATION NUMBER: US 07/549,587
 ; FILING DATE: 06-JUL-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; REGISTRATION NUMBER: 32,534
 ; REFERENCE/DOCKET NUMBER: A0496
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 454-3817
 ; TELEFAX: (215) 454-3808
 ; INFORMATION FOR SBO ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 27
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-323-430-14
 Query Match 27.7%; Score 1180.6; DB 4; Length 2662;
 Best Local Similarity 70.0%; Pctd. No. 2;9e-280;

Matches 1621: Conservative 0; Mismatches 644; Indels 24; Gaps 3;
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 Db 254 GCTCTGCGGACAGTGTGAGAGATCACTGCTGTGGAGGCGGATGACGTGTGGGAAA 313
 Oy 518 ACAATAGGACATCTTATTTGGGAGTCTTGACAGTAAAGAGGCGGACGGCTAGAAACT 577
 Db 314 GCAAGCGCCGCGCATACAGGGAGAGAGGGAGGGAGGAGTCCGTGGCGGACACT 373
 Oy 578 GCGCGCTGTAGCTCTTACTGCGAGTACAGCTGATGATAGATTAATCTTATATG 637
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Oy 2063 AGATGACCTTAAGACTTGTGTGTCATCGACCTACACAGCTGGCGAGAGCATGAGTACT 2122
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Search completed: December 11, 2002, 14:33:23
 Job time : 144 secs

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Oy 2660 CTGTCTTTTCTCCAGACCCATGCTTCCAGACCAAGTCCCTCTCAATATGCAACATAA 2719
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Oy 2720 CAGGCACTG 2728
Db 2528 TTGCAATG 2536

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ALIGNMENTS

RESULT 1

; GENERAL INFORMATION:

TITLE OF INVENTION: PRO

FILE REFERENCE: 689290-

CURRENT FILING DATE: 2/2/2018

PRIOR FILING DATE: 2000

PRIOR FILING DATE: 2000

PRIOR FILING DATE: 2000

PRIOR FILING DATE: 2000

PRIOR FILING DATE: 2000
PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 2000
PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER

PRIOR APPLICATION NUMBER

PRIOR APPLICATION NUMBER

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 293

TYPE: DNA

US-09-954-456-293

Query Match
Best Local Similarity

Matches 4268; Conserva

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Db 3301 GAGGTGCAAAAAATATCTTTTCTTCCAGAGAGAAATGATATACAGTTAATTTAATAAT 3360
Oy 3361 TGGTAAATATCAAAACATTAATATATGATGATGATGATGATGATGATGATGATGATG 3420
Db 3361 TGGTAAATATCAAAACATTAATATATGATGATGATGATGATGATGATGATGATGATG 3420
Oy 3421 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
Db 3421 ATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
Oy 3481 TTTGAAAAGAGATATTTATACATATATATGATGATGATGATGATGATGATGATGATG 3540
Db 3481 TTTGAAAAGAGATATTTATACATATATATGATGATGATGATGATGATGATGATGATG 3540
Oy 3541 TTGTTTAAATATGCTGTGTCAGAGATGATGATGATGATGATGATGATGATGATGATG 3600
Db 3541 TTGTTTAAATATGCTGTGTCAGAGATGATGATGATGATGATGATGATGATGATGATG 3600
Oy 3601 AAAAAATCATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
Db 3601 AAAAAATCATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3660
Oy 3661 CAAGCTCTAATCTGATCTCCAGATTAATATGATGATGATGATGATGATGATGATGATG 3720
Db 3661 CAAGCTCTAATCTGATCTCCAGATTAATATGATGATGATGATGATGATGATGATGATG 3720
Oy 3721 ATCCATTCCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
Db 3721 ATCCATTCCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3780
Oy 3781 GCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
Db 3781 GCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
Oy 3841 TTTGATATATGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
Db 3841 TTTGATATATGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
Oy 3901 TCAATGAAATATGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
Db 3901 TCAATGAAATATGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
Oy 3961 TTAAGAGATGCTTTCATATATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4020
Db 3961 TTAAGAGATGCTTTCATATATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4020
Oy 4021 TACATGCAAAATATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4080
Db 4021 TACATGCAAAATATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4080
Oy 4081 AAACAGCCAGTCACTTTCATATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4140
Db 4081 AAACAGCCAGTCACTTTCATATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4140
Oy 4141 TCTTTCAGAAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4200
Db 4141 TCTTTCAGAAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4200
Oy 4201 ATGTTTTCAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4260
Db 4201 ATGTTTTCAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4260
Oy 4261 AAAAAAA 4268
Db 4261 AAAAAAA 4268

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RESULT 2
US-09-954-456-1599

D5	421	TACGTCGCTGGCCGACAGGAGATCCCTACAGGTCGCCCTCCGTGAAAGATCCGCCGCTGG	480
D5	481	ATTCAGTTGACATAAGATGAGATGCGATCTACTTGGGACCAACATATAGAGACAGTGGTATATGGG	540
D5	481	ATTCAGTTGACATAAGATGAGATGCGATCTACTTGGGACCAACATATAGAGACAGTGGTATATGGG	540
D5	541	GAGTACCTGTGACAGATTAAGAGGCGCCACCGCTAGAGACATCGGGCCCTCTATAGCTATATATGCG	600
D5	541	GAGTACCTGTGACAGATTAAGAGGCGCCACCGCTAGAGACATCGGGCCCTCTATAGCTATATGCG	600
D5	601	ACTAGAGACTGATACAGGTGAATCTTGCTATCTCATGTGTATGTCAACAGATGCCATCTCTA	660
D5	601	ACTAGAGACTGATACAGGTGAATCTTGCTATCTCATGTGTATGTCAACAGATGCCATCTCTA	660
D5	661	TCCGAGATGATGATAGATGACACCGGATGATGGGAGAAATTTGTACATGGAGAACATTAAC	720
D5	721	AACACAGACAGACATATATGACCAACACAGAAAGATGGAAAGCGCTCCATCTCTGTG	780
D5	721	AACACAGACAGACATATATGACCAACACAGAAAGATGGAAAGCGCTCCATCTCTGTG	780
D5	781	CGTCGCGCAACACATGTCAAGTTTCCCTTCCGCGCGCGGGGGGGAACCAATGCAACATG	840
D5	781	CGTCGCGCAACACATGTCAAGTTTCCCTTCCGCGCGCGGGGGGGAACCAATGCAACATG	840
D5	841	CGCTGCTGTGAATAACGGGAAAGAGATTTACCGAGAGCATCCATTTGAGAGCTACACAGTA	900
D5	841	CGCTGCTGTGAATAACGGGAAAGAGATTTACCGAGAGCATCCATTTGAGAGCTACACAGTA	900
D5	901	CGAACAACAGCACATGAGACCTCATTTATGCAAGCTGTGTCCATCCATGCAAGGAAATTAAT	960
D5	901	CGAACAACAGCACATGAGACCTCATTTATGCAAGCTGTGTCCATCCATGCAAGGAAATTAAT	960
D5	961	ACCTGTGTGTGATGAGATGAAATACGAGTCCATCAATCAACAGCTACCCATGGATGTTGTG	1020
D5	961	ACCTGTGTGTGATGAGATGAAATACGAGTCCATCAATCAACAGCTACCCATGGATGTTGTG	1020
D5	1021	GAGCGATCGCCTACACGGGCGCATCTCCACAGCGGAGATCCCGCAATGTGCTCACAGTGG	1080
D5	1021	GAGCGATCGCCTACACGGGCGCATCTCCACAGCGGAGATCCCGCAATGTGCTCACAGTGG	1080
D5	1081	GTTCGAGAGACAGTGAAGTTGTCTCAAGCTTTTACAGTGTATGATGACCGGCCCATCTCAG	1140
D5	1081	GTTCGAGAGACAGTGAAGTTGTCTCAAGCTTTTACAGTGTATGATGACCGGCCCATCTCAG	1140
D5	1141	TGGATGACAGCACCTGTGAAAGAGAGGCGAGTAATACGGGCGCCAGCGGCTCCCTACCTC	1200
D5	1141	TGGATGACAGCACCTGTGAAAGAGAGGCGAGTAATACGGGCGCCAGCGGCTCCCTACCTC	1200
D5	1201	AGGCTTCTCAGAGGCGCCGCTGTTAACACACAGCGAACAAGATGAGAGTTCTCTATATT	1260
D5	1201	AGGCTTCTCAGAGGCGCCGCTGTTAACACACAGCGAACAAGATGAGAGTTCTCTATATT	1260
D5	1261	CGGAAATGATCTTTTGAAGAGCGCTGGGGATATACGTGCTTGGCGGATTCATATATGGG	1320
D5	1261	CGGAAATGATCTTTTGAAGAGCGCTGGGGATATACGTGCTTGGCGGATTCATATATGGG	1320
D5	1321	AATTCCTTCACTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1380
D5	1321	AATTCCTTCACTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1380
D5	1381	ACACACTTCCCAACATACCTGAGAGATACCATTTATCTGCATACAGAGCTCTTCTTAATGCC	1440
D5	1381	ACACACTTCCCAACATACCTGAGAGATACCATTTATCTGCATACAGAGCTCTTCTTAATGCC	1440
D5	1441	TGTATGTGTGATACAGTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1500
D5	1441	TGTATGTGTGATACAGTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1500
D5	1501	ACACGACAGCGGCTGTGACACAGCTGACCAAGATATCCCTTCGCGAGACAGATGATACA	1560
D5	1501	ACACGACAGCGGCTGTGACACAGCTGACCAAGATATCCCTTCGCGAGACAGATGATACA	1560

[illegible]

: OTHER INFORMATION: n equals a..t..c or c									
US-09-925-27-21									
Query Match	27.6%	Score 1177.2	DB 10:	Length 3726:					
DB 10:	Similarity	71.0%	Pos. No. 6:	Size 263:					
Matches 1608:	Conservative	3:	Mismatches 631:	Indels 24:	Gaps				
0y	481	ATCATGTGACATGAGAGTGGGGGACCTTGTGGGCGCCAAATAGACAGAGTCTATTGGG	540						
Dy	16	ATGACTGTGGTGTGGGAGGGGTGTGACGTGGGAAGACACCCGACACGAGG	75						
0y	541	ATGACTTTCGATATGAGGCGGACCTGTAGAGCTGCGCTGATGAGTCTGACTGCG	600						
Dy	76	AGAGAGTGGAGTGCAGGACTCTGTGCGCCGAGACTGGGCGCTATCTGCTGCTACG	135						
0y	601	AGTAGACTGTAGACAGTGAATCTGTGCTACTGATGATGTGACAGATGCGACATGCA	660						
Dy	136	AGACGCGCTGTGGGAGTGAACACGACTCTTCCCTCCAAATGTTTCATATGCTCTGCG	195						
0y	661	TGGCGATATGTGAGATGACACGCAATGCTGCGAAGATTTTGTCACTGACACATGAC	720						
Dy	196	TCTGGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	255						
0y	721	AGCA-----GAAACACATATCTGACACGACACACAAAGATGAAAG	785						
Dy	256	ACCAACCAACCGTATGCGGTACTGATGATGATGATGATGATGATGATGATGATGATG	825						
0y	766	CGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	815						
Dy	316	AATTCATGCTAGTCTGCGGCTGCGACAGATGATGATGATGATGATGATGATGATGATG	375						
0y	826	CCATGCCACATGAGTGGGTGCTGAAAGACGAGAGGTATAGAGAGAGATGCTGATT	885						
Dy	376	CCAAACCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	435						
0y	886	GGAGCTTCAAGATGAGACACGACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG	945						
Dy	436	GGAGCTTCAAGATGAGACACGACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG	495						
0y	946	GACAGGAAATTTATACGTGTGTGTGTGAGATGATGCGGTCTCATCATCACGCTAC	1005						
Dy	496	GACAGGAAATTTATACGTGTGTGTGTGAGATGATGCGGTCTCATCATCACGCTAC	555						
0y	1006	GACAGGAAATTTATACGTGTGTGTGTGAGATGATGCGGTCTCATCATCACGCTAC	1065						
Dy	556	CAGTGTGATGT	615						
0y	1066	AATGCTCTCCACAGT	1125						
Dy	616	AACAAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	675						
0y	1126	GAGGCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1185						
Dy	676	CAGGCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	735						
0y	1186	GAGGCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1245						
Dy	736	AAGTATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	795						
0y	1246	GAGTATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1305						
Dy	856	GATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	915						
0y	1366	AGCAAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1425						
Dy	916	GAGGCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	975						
0y	1426	GTCCTCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1485						

Dy	976	ACCTCTCCATCTCCAGGAGGCGGGGGGGTGCATCTCTCAGCAAGAGTAAGAGTGGTAC	10133
Dy	1486	AAGAGACCAATTCACAGACACCGACGCGCTGTGCACAACTGACACAAAGGTCTCCCTCTG	10134
Dy	1036	AAGAGAGATGATTAATTTTGGCGAGAGAGTGGTGTCTGACAGCTCAGCAACACCCCTCTGG	10145
Dy	1546	CGAGACAGGTATAAATTTTGGCGAGAGTGGTGTCTGACAGCTCAGCAACACCCCTCTGG	16051
Dy	1096	CGAGACAGGTATAAATTTTGGCGAGAGTGGTGTCTGACAGCTCAGCAACACCCCTCTGG	11551
Dy	1606	GTGAGGATTAACACAGCGCTCTCTTAAGGGCGAGACCCCATGTGTGGAGGGGTCTCC	16651
Dy	1156	GTTCGGCCATCACGGCTCTCTCTCCACAGT-----GGAGCTCCATGTGTAAGAGGGGTCTCT	12091
Dy	1666	GAGTATCAATTTCCACAGACACCCAAATTTGGATTTTCCAAAGATTTACGTACGTACGTGGC	17251
Dy	1210	CAGTATGAGGTTTCCCAAGACCGCTGTGGAGCTGTGGCTCGGAGACGAGCTGGTCTTAAGC	12691
Dy	1726	AACCCCTGTGGAGAGAGTTTGTCTTTGGCGACATGTGTCAATGGCGACACAGTGGGATTTAC	13781
Dy	1370	AACACCGCTGGAGAGAGCTCTCTCTCCGCGCGCTGTGAAGATTTGGAGATTTATGGCCACA	13821
Dy	1786	AAGACACCGCTGGAGAGAGCTCTCTCCGCGCGCTGTGAAGATTTGGAGATTTATGGCCACA	18451
Dy	1330	AAGGACAAACCCACACCGTGTGACACAAAGGGCTGTGAAGATTTGTAAGTGGAGCCACAA	13891
Dy	1846	GAGAAAGACCTTCTGATCTGTGTCTCAGATGCGAGATGATGAGGAATGATTTGGGAAACAC	19051
Dy	1390	GAGAAAGACCTTCTGATCTGTGTCTCAGATGCGAGATGATGAGGAATGATTTGGGAAACAT	14491
Dy	1506	AAGATATCTATTAATTTCTTTGGAGCTTCCACACAGATAGGGCTCTCTCTATCATATTT	19651
Dy	1450	AAGATATCTATTAATTTCTTTGGAGCTTCCACACAGATAGGGCTCTCTCTATCATATTT	15091
Dy	1866	GAGATATCTCTTAAGAGCACCTCTCGAGATACCTCTCGACACCGCCGAGGCGACCCGGGATG	20231
Dy	1510	GAGATATCTCTTAAGAGCACCTCTCGAGATACCTCTCGACACCGCCGAGGCGACCCGGGATG	15691
Dy	2026	GAGTACTCTGTATGACATTAACAGCTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	20891
Dy	1570	GAGTACTCTGTATGACATTAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	21571
Dy	2086	TCATGACCTACAGCTGT	21441
Dy	2146	CGAGATTTTACAGCGCAAAATTTGTTTGGTAAAGAAACATGTGTGTAATTTAGGAGAC	22051
Dy	1630	TCCTGCGCTACAGATGT	16891
Dy	1690	CGAGACCTGGACACCGAGATTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	17491
Dy	2206	TTTGTGACTGGCCAGAGATTTCAACATTAATACCTTTTCAAAAAGACACCAATTTGGGCGT	22651
Dy	1750	TTTGTGACTGGCCAGAGATTTCAACATTAATACCTTTTCAAAAAGACACCAATTTGGGCGT	18091
Dy	2266	CTTTCACCTACAGATGT	23251
Dy	1810	CTTTCACCTACAGATGT	18691
Dy	2326	GATGTGTGTCTGTGGAGGTGTTAATGTGGAGATCTTTCACCTTAAAGGGGCTGTCCCTTAC	23851
Dy	1870	GATGTGTGTCTGTGGAGGTGTTCCTTGTGGAGATCTTTCACCTTGTGGGGCTGTCCCTTAC	19291
Dy	2386	CGAGAGATTTCCCTGTGAGAGAACTTTTAAAGCTGTCAAGAGAGACACAGAAATGATATAG	24451
Dy	1930	CGCGGT	19891
Dy	2446	CCACCCATCTGACACAGACCTGTACATGATGTAGGAGAACTTTGTGCAATCTAGTGTCC	20491
Dy	1990	CCGAGATATGT	20541
Dy	2506	TCCGAGAGACCAAGTGTGAAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	25651
Dy	2050	TCCGAGAGACCAAGTGTGAAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	21091

[illegible]

[illegible]

Db 182 CCGTAAACATGTCAGTGGGAGTCTTTCATCTGCTGATGCTGTCACCATGACACCT 241
Oy 326 TGTCCCTGGGCGGCGCTGCTCAGCTTATTGTTGAGGATACACCATATGACGCGAAGAC 385
Db 242 TGTCCCTGGGCGGCGCTGCTCAGCTTATTGTTGAGGATACACCATATGACGCGAAGAC 301
Oy 386 CACCAACCAATACCAATCTCTCAACCCAGAAAGTATGCTGCTGCGCCAGGAGGTGCG 445
Db 302 CACCAACCAATACCAATCTCTCAACCCAGAAAGTATGCTGCTGCGCCAGGAGGTGCG 361
Oy 446 TAGAGGTGCGCTGCTGTTGAAAGATATGCGCGCTGATCATCTGATGATAGATGGGTG 505
Db 362 TAGAGGTGCGCTGCTGTTGAAAGATATGCGCGCTGATCATCTGATGATAGATGGGTG 421
Oy 506 ACTTGGGCGCCCAACATAGGACAGTGTCTATTGTTGGGAGTACTTGGACATTAAGGCGCCCA 565
Db 422 ACTTGGGCGCCCAACATAGGACAGTGTCTATTGTTGGGAGTACTTGGACATTAAGGCGCCCA 481
Oy 566 GCGCTCAAGACATCGCGCTGCTATGCTGTATCTGCGATGAGACATGTACAGATGGAACCT 625
Db 482 GCGCTCAAGACATCGCGCTGCTATGCTGTATCTGCGATGAGACATGTATGACAGTGAACCT 541
Oy 626 GGTACTTCATGCTGTAATGTCACAGATGTCATCTATCCGAGAGTATGATGATGACACCC 685
Db 542 GGTACTTCATGCTGTAATGTCACAGATGTCATCTATCCGAGAGTATGATGATGACACCC 601
Oy 686 ATGTGCGGAAGATTTGTCTGATGCGAAGCAATGACAAAG 728
Db 602 ATGTGCGGAAGATTTGTCTGATGCGAAGCAATGACAAAG 644

RESULT 7
us-09-954-556-3. std. rnpb
Sequence 82: Application US/09728952
Patient No. US2020111302A1
GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Zhou, Ping
: APPLICANT: Goodrich, Kyle
: APPLICANT: Liu, Jiezhong
: APPLICANT: Asmadi, Vahid
: APPLICANT: Wang, Jian-Bul
: APPLICANT: Wang, Duntul
: APPLICANT: Yemazaki, Vicki
: APPLICANT: Ujwal, Manusha L.
: APPLICANT: Dhanraj, Radoye T.
: TITLE OF INVENTION: No. US2020111302A1el Nucleic Acids and
: TITLE OF INVENTION: Polypeptides
: FILE REFERENCE: 799
: CURRENT APPLICATION NUMBER: US/09/728,952
: NUMBER OF SEQ ID NOS: 101
: SOFTWARE: pL-Fl-Genes Version 2.0
: SEQ ID NO 82
: LENGTH: 2184
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (40)..(2124)
US-09-728-952-82

Query Match 15.0% Score 640.6, DB 10: Length 2184,
E-Value 1.0e-138, Ident 73.3%, Pos 16-138,
Matches 036: Conservative 0: Mismatches 259: Indels 6: Gaps 1:
Db 1614 AACCAACGCTCTCTTCACACGCGACACCCCATGCTGGAGGAGTCTCCAGATATCA 1673
Oy 1614 AACCAACGCTCTCTTCACACGCGACACCCCATGCTGGAGGAGTCTCCAGATATCA 1673
Db 1023 GCGAAGCTCTCTCTA-----GGGAGAGGCGCCACAGCTGGCAATATCTCGAAGCTCA 1076

Oy 1674 ACTTCCAGAGAGACCAAAATGGAGATTTCACAGAGATACCTGACACTGTGCGACACCGCT 1733
Db 1077 GGTGCTCTCGACCAACCAATGGAGACTGTCTGTGGCGCGGCTGACACTGTGGACACCGCT 1136
Oy 1734 GGGAGAGAGTGTGCTGGGCAAGTGTGATATGGCGAGACAGTGGCAATTTGACAAAGACAA 1793
Db 1137 TGGAGAGAGTGTGCTGGGCAAGTGTGATATGGCGAGGAGTGTGCGACGTGGACAAAGACCA 1196
Oy 1794 GGGAGAGAGTGTGCTGGGCAAGTGTGATATGGCGAGGAGTGTGCGACGTGGACAAAGACCA 1853
Db 1197 GGGAGAGAGTGTGCTGGGCAAGTGTGATATGGCGAGGAGTGTGCGACGTGGACAAAGACCA 1286
Oy 1854 CCTTCTGATCTGTGTCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1913
Db 1287 CCTTCTGATCTGTGTCAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1316
Oy 1914 CTTAAATCTCTTGGACCTGCGACAGATGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1973
Db 1317 CATCAACCTCTGTGGGCGCTGACACAGAGAGGCGGCGCTGTAGTGTGTGTGATGATGCT 1376
Oy 1974 CTTAAAGGCAACCTGCGACAGATGAGTGGCTGCTGCGACCGGAGGCGACCGCGGATGATGCT 2033
Db 1377 GCGCAAGGCTTACCTGTGCGGAGTGTCTGTGCGGCGCGCGCGCGCGCGCGCGGATGATGCT 1436
Oy 2034 CTTAACTTATACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2093
Db 1437 CTTAACTTATACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1496
Oy 2094 CTTAACTTATACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2153
Db 1497 CTTAACTTATACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556
Oy 2154 AGCAAGCAAGATTTGTGTAACAGAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 2213
Db 1557 GCTTGTGCGCAATGTGCTGTGTGACAGAGACAGATGATGATGATGATGATGATGATGATGAT 1616
Oy 2214 CCGCAAGATATGTCACAAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2273
Db 1617 GAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1676
Oy 2274 GAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2333
Db 1677 GAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736
Oy 2334 GTCTTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2393
Db 1737 GTCTTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1796
Oy 2394 TGGCGTGGAGAACTTTTAAGCTGTGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2453
Db 1797 CCTGTGGAGAGCTCTCAAGCTGTGTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1856
Oy 2454 CTGACCAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2513
Db 1857 CTGACCAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1916
Oy 2514 AGCAAGTTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2573
Db 1917 GCGCACCTCTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1976
Oy 2574 GCAATCTTGTGAGCTCAGCAACCTGTGCAAGATATTCACAGATGATGATGATGATGATGATGAT 2633
Db 1977 CCAATGTCAGAGCTGTGCGCGGCGCTGTGCAAGATATTCACAGATGATGATGATGATGATGATGAT 2036
Oy 2634 AAGTCTCTGCTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2693
Db 2037 CAGCTCAAGCTCTCTAGGAGAGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2096
Oy 2694 A 2694
Db 2097 A 2097


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Sequence 250, Application US/10106605
Patent No. US20020160934A1
GENERAL INFORMATION:
  INVENTOR: Drosophila, Julie
  APPLICANT: Spam Lynn
  APPLICANT: Bechmann, Jane
  APPLICANT: Kamaid, Kim
  TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
  FILE REFERENCE: 31133B
  CURRENT APPLICATION NUMBER: US/01/09,605
  PRIORITY DATE: 2001-01-16
  PRIOR APPLICATION NUMBER: US 09/761,142
  PRIOR FILING DATE: 2000-01-14
  NUMBER OF SEQ ID NOS: 361
  SOFTWARE: PatentIn Ver. 2.1
  LENGTH: 2782
  TYPE: DNA
  ORGANISM: Drosophila melanogaster
US-10-108-605-250

Query Match
Best Local Similarity 6.4%; Score 275.2; DB 9; Length 2782;
Matches 347; Conservative 0; Mismatches 333; Indels 42; Gaps 3;

OY 1650 GCTGGCAGGGGCTCCGAGATGAGTACCTTCGAGAGCCCAAGATGGAGTTCGAGAGCA 1709
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1246 GCGGCTCATTCATGATATGAAATTCCTCGGACATCGAGATGCAATGCCAGAG 1305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1710 TAAGCTGACATGGGCAAGCCCTCGAGAGAGTGTGCTTGGGCAATGGTATGCGCGA 1769
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1306 TCAATTGTGACTGGGAGTCACTTTGGAGAGAGTCTTTGAGAGATGATGATGAGGGA 1365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1770 AGCAGTGGAGATGACAAAGACACCCAGAGAGGCGGTACCGCTGCGAGAGATGTT 1829
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1366 GGTCA-----ATAATGCAATGTGTGCGGTGAAATGGT 1398
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1830 GAAGATGATGCGCAGAGAAACCTTTCATGATGCTGTGTCAGAGATGAGATGATGAA 1889
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1399 GAGAGAGAGACAGAGAGTGAACATGCTGACCTGAGCGAGAAATGAGAGATGAA 1458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1890 GATGATGGGAAACACAGATATCAATATCTTTGGAGACCTGCGACAGAGATGGGCG 1949
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1459 GATGATGGGAGCATCATATATATTTAACGCTAGCTGGTGCAGTAAATGGTCC 1518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1950 TCTCTATGTCATAGTGAATGATGCTCTTAAAGCAACCTCCAGAAATGCT----- 2000
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1519 GCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1578
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2001 ----CGAGCCGAGAGCGACCGGAGATGAGATGCTCTTATGACATTAACGATGTTCTGGA 2057
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1579 TCGCGATCCGAGAGGATGACAGAGGAGAGCTCCACACCGCGCATCCGACCAAGC 1638
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2058 GAGAGATGACCTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2117
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1639 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1698
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2118 GTATCTGCTTCGCAAAATGATATGATGATGATGATGATGATGATGATGATGATGATG 2177
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1699 GTATTTGGGCTCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1758
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2178 AGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1759 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1818
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2238 CTATTAACAAAAAGACACATGAGGCGCTTCATGATGATGATGATGATGATGATGATG 2297
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1819 TTACTATCGAAGAGACAGATGAGGATGATGATGATGATGATGATGATGATGATGATG 1878
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 2298 GTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2357
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```

```

RESULT 14
US-09-814-950-3
Sequence 3, Application US/09814950
Patent No. US20020137130A1
GENERAL INFORMATION:
  INVENTOR: Wei, Ming-Hui et al
  APPLICANT:
  TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND
  FILE REFERENCE: C1001174
  CURRENT APPLICATION NUMBER: US/09/814,950
  PRIORITY DATE: 2001-03-23
  NUMBER OF SEQ ID NOS: 4
  SOFTWARE: FastSD for Windows Version 4.0
  LENGTH: 33239
  TYPE: DNA
  ORGANISM: Human
  FEATURE:
  NAME/KEY: m1sc_feature
  LOCATION: (1)..(33239)
  OTHER INFORMATION: n = A,T,C or G
US-09-814-950-3

Query Match
Best Local Similarity 6.4%; Score 271.2; DB 10; Length 33239;
Matches 273; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 377 CAAAGAGCCACACACAAATTCCTGATACAGAGATGATGATGATGATGATGATGATG 436
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DB 29850 CTCAGAGCCACACACAAATTCCTGATACAGAGATGATGATGATGATGATGATGATG 29909
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 437 GGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 29910 GGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 29969
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 497 ATGGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 29970 ATGGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 30029
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 557 AGGGGAGCCAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 30030 AGGGGAGCCAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 30089
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 617 GTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 30090 GTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 30125
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RESULT 15
US-09-731-872-128
Sequence 128, Application US/09731872
Patent No. US20020102604A1

```

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: GENERAL INFORMATION:
: APPLICANT: Dumas MLine Edwards, Jean Baptiste
: APPLICANT: Bouguetelarel, Lydie
: TITLE OF INVENTION: POTENTIAL HUMAN CDNNS ENCODING POTENTIALLY SECRETED PROTEINS
: FILE REFERENCE: 78. US3.REG
: CURRENT APPLICATION NUMBER: US/09/731.872
: PRIOR APPLICATION DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 60/169,629
: PRIOR FILING DATE: 1999-12-08
: PRIOR APPLICATION NUMBER: US 60/187,470
: PRIOR FILING DATE: 2000-03-06
: NUMBER OF SEQ ID NOS: 482
: SOFTWARE: Patent.pm
: SEQ ID NO 128
: LENGTH: 618
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 179..427
: NAME/KEY: s19.peptide
: LOCATION: 179..298
: OTHER INFORMATION: von Heljne matrix
: OTHER INFORMATION: score 7.72883276007822
: OTHER INFORMATION: seq CLVWYVMTLSLA/RP
: US-09-731-872-128

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Query Match          6.1%; Score 262.4; DR 10; Length 618;
Best Local Similarity 99.6%; Pred. No. 2.3e-51;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 120 CAGGTGACTGCACGACGACGCGAGCGGCTTCGTGAGCCACCGAGCGCTGAAGGC 179
DB 82 CAGGTGACTGCACGACGACGCGAGCGGCTTCGTGAGCCACCGAGCGCTGAAGGC 141
OY 180 ATTGCGCGTAGTCATGCCGTAGAGAGAGTGTGCAGATGGATTAACTGCACATGGAG 239
DB 142 ATTGCGCGTAGTCATGCCGTAGAGAGAGTGTGCAGATGGATTAACTGCACATGGAG 201
OY 240 ATTGCAAGAGACCGGGGATTGGTACGTAACTGTCAGTGGGGTCTGTTTCATCTG 299
DB 202 ATTGCAAGAGAGACCGGGGATTGGTACGTAACTGTCAGTGGGGTCTGTTTCATCTG 261
OY 300 CCTGGTGTGGTACCATGGCAACCTGTGTCCCTGGCCGGGGCCCTCTTCAGTTAGTTGA 359
DB 262 CCTGGTGTGGTACCATGGCAACCTGTGTCCCTGGCCGGGGCCCTCTTCAGTTAGTTGA 321
OY 360 GGAATCCACATTTAGAGCCGAAGA 383
DB 322 GGAATCCACATTTAGAGCCGAAGA 345

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Search completed: December 11, 2002, 17:40:36
Job time : 388 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:19:57 ; Search time 3671 seconds

(without alignments)
18825.294 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 1 cccagagaccaccccttcgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY/JNC

Gapop 10.0 ; Gapext 1.0

Searched: 16154066 segs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

EST:
1: em.estab:*
2: em.esthum:*
3: em.estlin:*
4: em.estnu:*
5: em.estol:*
6: em.estl1:*
7: em.estl2:*
8: em.estl3:*
9: gb.est1:*
10: gb.est2:*
11: gb.est3:*
12: gb.est4:*
13: gb.est5:*
14: gb.est6:*
15: em.estom:*
16: em.estom1:*
17: gb.gss:*
18: em.gss.hum:*
19: em.gss.hmv:*
20: em.gss.pln:*
21: em.gss.tun:*
22: em.gss.hum:*
23: em.gss.hum:*
24: em.gss.mus:*
25: em.gss.other:*
26: em.gss.pro:*
27: em.gss.tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best hit being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	840.6	19.7	885 14	BQ438964
2	765.6	17.9	883 9	A1127918
3	762.8	17.9	803 9	BQ123037
4	731.4	17.1	987 9	BQ879891
5	707.4	16.6	834 12	BQ698600
6	688.2	16.1	747 9	A1081876

Result No.	Score	Query Length	DB ID	Description
1	840.6	19.7	885 14	BQ438964
2	765.6	17.9	883 9	A1127918
3	762.8	17.9	803 9	BQ123037
4	731.4	17.1	987 9	BQ879891
5	707.4	16.6	834 12	BQ698600
6	688.2	16.1	747 9	A1081876

FEATURES

source

1. 885

ALIGNMENTS

RESULT 1

LOCUS BQ438964

DEFINITION BQ438964.1 GI:21178040

ACCESSION BQ438964

VERSION BQ438964.1

KEYWORDS

SOURCE

ORGANISM Homo sapiens

REFERENCE

AUTHORS NIH-MGC http://mhc.ncl.nih.gov/

TITLE National Institutes of Health/Mammalian Gene Collection (MGC)

COMMENT

1 (bases 1 to 885)

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUMI)

CDNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found at: <http://image.llnl.gov>

Plate: LMA13218 row: h column: 01

High quality sequence spot: 770.

Location/Qualifiers

1. 885


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Db 587 CACCTCTGCAAGATATTCACCTAGTTACCTGACACAGAAAGTCTGTTCTCAGCA 528
Oy 2653 GATGATTCGTGTTTTCTTCAGACCCATGCTTACGAAACCATGCTTCTTCATATCA 2712
Db 5527 GATGATTCGTGTTTTCTTCAGACCCATGCTTACGAAACCATGCTTCTTCATATCA 468
Oy 2713 CACATTAAGGAGC-AAGTGTAAAGATGAATGACGTGTCTCCCTGCTCCCAAGAGCA 2771
Db 467 CACATTAAGGAGCAGTGTAAAGATGAATGACGTGTCTCCCTGCTCCCAAGAGCA 408
Oy 2772 GCAATGGGACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 2831
Db 407 GCACCTGGGACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 348
Oy 2832 ACTGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2891
Db 347 ACTGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 288
Oy 2892 ATTTATATACGTGAAACCTGTAATCTCCGACAGAGCAAGAAAGTTCTTGACAGAT 2951
Db 287 ATTTATATACGTGAAACCTGTAATCTCCGACAGAGCAAGAAAGTTCTTGACAGAT 228
Oy 2952 GGACGTGCAACACCATCATGTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3011
Db 227 GGACGTGCAACACCATCATGTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 168
Oy 3012 GTAGAGCTCAAGGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3071
Db 167 GTAGAGCTCAAGGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 108
Oy 3072 GATTTATGTGACGACACCTACCTACGAGCAAGAAATGAGTATAGGTGCTGATGATGT 3131
Db 107 GATTTATGTGACGACACCTACCTACGAGCAAGAAATGAGTATAGGTGCTGATGATGT 48
Oy 3132 AATGATATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3175
Db 47 AATGATATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4

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RESULT 3
LOCUS NT2RP3 Homo sapiens cDNA clone NT2RP3004190 5', mRNA

DEFINITION
sequence.

ACCESSION
AJ132307

VERSION
AJ132307.1 GI:1092661

SOURCE
EST.

ORGANISM
Homo sapiens

EXTRACTOR
Eukaryotic Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 803)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Makematsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Ishiguro,T. cDNA project

TITLE
JOURNAL
COMMENT
Contact: Takao Isegai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3575
Fax: 81-438-52-3586
E-mail: tisegai@helix.co.jp
Helix human cDNA project: 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="NT2RP3004190"

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Best Local Similarity 98.4%; Pred. No. 2,8e-151;
Matches 790; Conservative 0; Mismatches 10; Indels 3; Gaps 2;
BASE COUNT 231 a 193 c 210 g 166 t 3 others
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/cell_type="teratocarcinoma"
/cell_line="NT2"
/Note="Vector: pMERISFL3; mRNA from NT2 neuronal precursor
cells after 2 weeks retinoic acid (RA) induction."

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Query Match 17.9% Score 762.8; Db 9; Length 803;
Best Local Similarity 98.4%; Pred. No. 2,8e-151;
Matches 790; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

1434 AATGCCCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1493
Db 1 AATGCCCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Oy 1494 AAGCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1553
Db 61 AAGCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 120
Oy 1554 GATTAACGTTTGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1613
Db 121 GATTAACGTTTGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Oy 1614 AACAACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1673
Db 181 AACAACAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Oy 1674 ACTTCCAGAGACCCAAATGGAGTTTCCAGAGATGATGATGATGATGATGATGATGAT 1733
Db 241 ACTTCCAGAGACCCAAATGGAGTTTCCAGAGATGATGATGATGATGATGATGATGAT 300
Oy 1734 GCGAGAAAGGTGCTTGGCAGAGGTGATGATGATGATGATGATGATGATGATGATGAT 1793
Db 301 GCGAGAAAGGTGCTTGGCAGAGGTGATGATGATGATGATGATGATGATGATGATGAT 360
Oy 1794 GCCCAGAGGCGGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1853
Db 361 GCCCAGAGGCGGTGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Oy 1854 CCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1913
Db 421 CCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Oy 1914 CATTAAATCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1973
Db 481 CATTAAATCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Oy 1974 CTTTAAAGCAACCTCCGAGATACCTCCAGACCCGAGGCGACCCGAGATGATGATGAT 2033
Db 541 CTTTAAAGCAACCTCCGAGATACCTCCAGACCCGAGGCGACCCGAGATGATGATGAT 600
Oy 2034 CTTTAAAGCAACCTCCGAGATACCTCCAGACCCGAGGCGACCCGAGATGATGATGAT 660
Db 601 CTTTAAAGCAACCTCCGAGATACCTCCAGACCCGAGGCGACCCGAGATGATGATGAT 660
Oy 2094 CTTTAAAGCAACCTCCGAGATACCTCCAGACCCGAGGCGACCCGAGATGATGATGAT 2133
Db 661 CTTTAAAGCAACCTCCGAGATACCTCCAGACCCGAGGCGACCCGAGATGATGATGAT 719
Oy 2194 AGCGAGCAAGATGTTTGGTACAGAAAAAGATGATGATGATGATGATGATGATGATGAT 2211
Db 720 AGCGAGCAAGATGTTTGGTACAGAAAAAGATGATGATGATGATGATGATGATGATGAT 779
Oy 2212 CTTCCCAAGATATCAACATAT 2234
Db 780 TCGACAGAGATATCAACATTT 802

RESULT 4
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DEFINITION ACBNC008F_8232182 Lupsk1_dorsal_root_ganglion Homo sapiens cDNA

clone IMAGE:6182720 5', mRNA sequence.
 B0879891
 VERSION B0879891.1 GI:22271899
 KEYWORDS EST
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Cetrarchi; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 987)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished 1997, Krausberg, Ph.D.
 COMMENT Email: cgep@b-ferrell.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://lml1559.rockefeller.edu/
 Plate: LML1559 row: c column: 09
 High quality sequence stop: 645.
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 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="DH10B"
 /note="Vector: pRW-SPO6 (Life Technologies); Site:1:
 Approx. 1 kb; CDNA made by oligo-dT priming
 5'-TCGACCAAGCGGTCG-3' and
 5'-GACTGATTTACATCCACGCGGCGCT(13)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies. 180 g 304 c

BLAST COUNT 300 a 203 c 304 c
 ORIGIN
 Query Match 17.1%; Score 731.4; DB 14; Length 987;
 Best Local Similarity 94.5%; Pred. No. 1.3e-144;
 Matches 791; Complement 0; Mismatches 41; Indels 5; Gaps 3;

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 Db 11 CTTGGACGCGACACTCTGCAAGATATTCACCTACCTGACAGAGAGTTC 70
 0y 2640 TTTGTTCTAGAGATGATTTCTGTTCTCGACAGCCCATCCCTTACGACCATGCT 2659
 |||||||
 Db 71 TTTGTTCTAGAGATGATTTCTGTTCTCGACAGCCCATCCCTTACGACCATGCT 130
 0y 2700 TCCCTCATGATCCACATTAAGCGGAGTTAAACGATGATGATGATGATGATGATG 2759
 |||||||
 Db 131 TCCCTCATGATCCACATTAAGCGGAGTTAAACGATGATGATGATGATGATGATG 190
 0y 2760 CCMAACGAGACACACTGGGAACTAGCTACCTGACGAGGAGACATCCCTCCACAG 2819
 |||||||
 Db 191 CCMAACGAGACACACTGGGAACTAGCTACCTGACGAGGAGACATCCCTCCACAG 250
 0y 2820 CTTGGATGTCGACATCTGATTAATGATGAGAGAGAAATATATGGAAGATACAG 2879
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 Db 281 CTTGGATGTCGACATCTGATTAATGATGAGAGAGAAATATATGGAAGATACAG 310
 0y 2880 ATATGCTAAAGATTATACATTTGAAACCTGTAACTCTCCCGACGAGAGAGAGAGT 2939
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 Db 311 ATATGCTAAAGATTATACATTTGAAACCTGTAACTCTCCCGACGAGAGAGAGAGT 370

0y 2940 TTTGACACAGTGCATGTCACACACACACATGTAACCTGTCACCGGCTGCCTTC 2999
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 Db 371 TTTGACACAGTGCATGTCACACACACACATGTAACCTGTCACCGGCTGCCTTC 430
 0y 3000 GCGTGGACACAGTGCATGTCACACACACACATGTAACCTGTCACCGGCTGCCTTC 3059
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 Db 431 GCGTGGACACAGTGCATGTCACACACACACATGTAACCTGTCACCGGCTGCCTTC 3199
 0y 3060 ATATGCTAAAGATTATACATTTGAAACCTGTAACTCTCCCGACGAGAGAGAGT 3119
 |||||||
 Db 491 ATATGCTAAAGATTATACATTTGAAACCTGTAACTCTCCCGACGAGAGAGAGT 550
 0y 3120 CTTGACATGATGTAATATATGTAATATGTAATATATATATATATATATATATATAT 3179
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 Db 551 CTTGACATGATGTAATATATGTAATATGTAATATATATATATATATATATATATAT 610
 0y 3180 TTTATTTTGTATGATATTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3238
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 Db 611 TTTATTTTGTATGATATTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 670
 0y 3239 TTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3298
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 Db 671 TTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 730
 0y 3299 CAGAGCTGAGAAATACCTT--GCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 3354
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 Db 731 CAGAGCTGAGAAATACCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 790
 0y 3355 ATAAATGCTAAATATACAAACATTAATGATGATGATGATGATGATGATGATGAT 3411
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 Db 791 ATAAATGCTAAATATACAAACATTAATGATGATGATGATGATGATGATGATGAT 847

RESULT 5
 LOCUS B6598600
 DEFINITION 834 bp mRNA linear EST 07-MAY-2001
 602658361P2 NCL_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:480163 5',
 mRNA sequence.
 ACCESSION B6598600
 VERSION B6598600.1 GI:13966051
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Cetrarchi; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 834)
 NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgep@b-ferrell.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA
 Sequenced by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://lml10694.rockefeller.edu/
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 High quality sequence start: 7
 High quality sequence stop: 833.
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 /clone_lib="NCL_CGAP_Skn3"
 /lab_host="DH10B (71 phage-resistant)"
 /note="Origin: skin; Vector: pRW-SPO6; Site:1: NCI;
 Site:3: Salt; Cloned unidirectionally. Primer:
 Average insert size 1.3kb. Library constructed by Life
 Technologies. Note: This is a NCL_CGAP Library."

BASE COUNT 237 a 201 c 200 g 196 t
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 Query Match 16.6% Score 707.4; DB 12; Length 834;
 Best Local Similarity 97.0%; Pval. No. 1.6e-139;
 Matches 785; Conservative 0; Mismatches 16; Indels 8; Gaps 6;
 Oy 2179 GAGAAAGATGTATGA--AATAGCAGACTTTGTGACTGCGCA-GAGATATCAATAT 2235
 Oy 27 GATACAGATGTATGA--AATAGCAGACTTTGTGACTGCGCA-GAGATATCAATAT 86
 Oy 2235 GACATATCAAAAAGACCAAGCATAGGCGGCTCCAGTCAAGAGATGCTCCAGAGCC 2235
 Db 87 GACATATCAAAAAGACCAAGCATAGGCGGCTCCAGTCAAGAGATGCTCCAGAGCC 146
 Oy 2236 CTTGTTGATAGATATACACTATCATAGATGTCTGGTCTCTGGGCTTTATATGTG 2335
 Db 147 CTTGTTGATAGATATACACTATCATAGATGTCTGGTCTCTGGGCTTTATATGTG 206
 Oy 2356 GAGATCTTCACTTTAGAGGGGCTCGCCGCTACCGAGAGATTCGCTGAGACTTTTAA 2415
 Db 207 GAGATCTTCACTTTAGAGGGGCTCGCCGCTACCGAGAGATTCGCTGAGACTTTTAA 266
 Oy 2416 CTGCTAAGAGAGAGACAGATATGATTAAGCCAGCATGCGACCAAGCATGTATCAT 2475
 Db 267 CTGCTAAGAGAGAGACAGATATGATTAAGCCAGCATGCGACCAAGCATGTATCAT 326
 Oy 2476 ATGATAG 2535
 Db 327 ATGATAG 386
 Oy 2536 GAAAGCTTGATGCAATTCCTCACTGATCTGACAGCATAGATAGATAGTACTGACCTAGCA 2595
 Db 387 GAAAGCTTGATGCAATTCCTCACTGATCTGACAGCATAGATAGATAGTACTGACCTAGCA 446
 Oy 2596 CCGTCTGAGACAGATATACCTAGATTCACCTGAGACAGAGAGATTCCTGCTAGAGAT 2655
 Oy 447 CCGTCTGAGACAGATATACCTAGATTCACCTGAGACAGAGAGATTCCTGCTAGAGAT 505
 Oy 2656 GATTCGCTTTTCTCGAGAGCCAGATGCGTCAAGCATAGCTTCTGCTAGATTCAGAC 2715
 Db 506 GATTCGCTTTTCTCGAGAGCCAGATGCGTCAAGCATAGCTTCTGCTAGATTCAGAC 565
 Oy 2716 AATAAGCGAGTGTAAACATGATAGTACGTGCTGCTGCTCCCAAGAGAGAGAGAC 2775
 Db 566 AATAAGCGAGTGTAAACATGATAGTACGTGCTGCTGCTCCCAAGAGAGAGAGAC 625
 Oy 2776 TGGGACCTAGCTACACTGACAGAGAGACATCCCTCCAGAGCTTTGCTCTGCACT 2835
 Db 626 TGGGACCTAGCTACACTGACAGAGAGACATCCCTCCAGAGCTTTGCTCTGCACT 684
 Oy 2836 GATATATGATCAGAGAGAGATTAATTAATGGA--AAGTAATCAGCATATGCTGTAAGAT 2893
 Db 685 GATATATGATCAGAGAGAGATTAATTAATGGA--AAGTAATCAGCATATGCTGTAAGAT 744
 Oy 2894 TTAATCAGCATATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2952
 Db 745 TCAATPAAAGTTGAAACCTTGTAATCTTCCCGAGAGAGAGAAAGAGTTTCTGAGACAGT 804
 Oy 2953 GACTGCCAG 2981
 Db 805 GACTGCCAG 833
 RESULT 6
 A1081876/c A1081876 747 bp mRNA linear EST 24-SEP-1998
 DEFINITION oy77a01.x1 Soares_NHHPU.S1 Homo sapiens cDNA clone IMAGE:1662312
 3 similar to gb:M87701 FIBROBLAST GROWTH FACTOR RECEPTOR 2
 ACCESSION A1081876
 VERSION A1081876.1 GI:3418668
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE PubMed 11609427
 AUTHORS NC-CAP http://www.ncbi.nlm.nih.gov/ncicgap/
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT Robert Strausberg, Ph.D.
 EMAIL: capgs-remail@nih.gov
 NOTE: cDNAs available royalty-free through LNC; contact the
 IMAGE Consortium (http://image.llnwd.net) for further information.
 INSERT LENGTH: 1152 Std Error: 0.00
 SEQ PRIMER: 40m3 fwd. 5' from Amersham
 High quality sequence stop: 459.
 LOCATION/Qualifiers
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 /clone="IMAGE1662312"
 /clone_lib="Soares_NHHPU.S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="organ: mixed (see below); Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Sma I; Site 3: Xba I; Site 4: Not I; DNA from three
 normalized libraries (melanocyte 2NHM,
 NHHPU, and fetal heart NHHPU) were mixed, and as circles
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 were labeled with 32P and 48486-489475
 340488-345479 and 48486-489475
 137 c 144 g 217 t 4 others
 BASE COUNT 245 a 245 c 144 g 217 t 4 others
 ORIGIN
 Query Match 16.1% Score 688.2; DB 9; Length 747;
 Best Local Similarity 97.8%; Pval. No. 1.9e-135;
 Matches 727; Conservative 0; Mismatches 12; Gaps 3;
 Oy 3493 AATTATTCATATATACATATTTGGGGAAGATAGATTGATTTGCTGTTAAAT 3552
 Db 743 AATTATTCATATATATGCTATTTGGGGAAGATAGATTGATTTGCTGTTAAAT 684
 Oy 3553 GCTGCTGTACAGAGATTTCTTACAGCTCTT-AAATGCCCATATTAAGAGCACTT 3611
 Db 683 GCTGCTGTGTACAGAGATTTCTTACAGCTCTT-AAATGCCCATATTAAGAGCACTT 624
 Oy 3612 CATAGAGAGGCTTTCAATTTGGTGGCAACCGCTGCTATGTCGTCAAGAGCTGTAC 3671
 Db 624 CATAGAGAGGCTTTCAATTTGGTGGCAACCGCTGCTATGTCGTCAAGAGCTGTAC 684
 Oy 623 CATAGAGAGGCTTTCAATTTGGTGGCAACCGCTGCTATGTCGTCAAGAGCTGTAC 564
 Oy 3672 TGGAGCTTCCAGATTAATGATGATACAGGCTCTCTTAAGAGATGCTTATTCCTCT 3731
 Db 563 TGGAGCTTCCAGATTAATGATGATACAGGCTCTCTCTTAAGAGATGCTTATTCCTCT 3791
 Oy 3732 TGGAGCTTCCAGATTAATGATGATACAGGCTCTCTCTTAAGAGATGCTTATTCCTCT 3791
 Db 503 TGGAGCTTCCAGATTAATGATGATACAGGCTCTCTCTTAAGAGATGCTTATTCCTCT 444
 Oy 3792 GCTTCTGAGTGTGACATTAATGATTAAGCTG-ATTCTCTTACGATGATTTGATTAATG 3850
 Db 443 GCTTCTGAGTGTGACATTAATGATTAAGCTG-ATTCTCTTACGATGATTTGATTAATG 384
 Oy 3851 GCTTCTGAGTGTGATTTTGGTGGAGAGAGCTTGAAGATTCCTCAAGCTCCAGAGAA 3908
 Db 383 GCTTCTGAGTGTGATTTTGGTGGAGAGAGCTTGAAGATTCCTCAAGCTCCAGAGAA 324
 Oy 3909 AATTGAAACAGAGATTTGCTGCTGATAGTTTGGGATAGCTGATTCCTTTTAAAGGGA 3968
 AATTGAAACAGAGATTTGCTGCTGATAGTTTGGGATAGCTGATTCCTTTTAAAGGGA

Db 323 AATTGAACACAGAGTTGTTCTGTGATAGTATTTGGGAGTACGTGTCATCTTTTAAGGGA 264
 Db 3969 TTGCTTCATCATATTCGTGACAGACCTGACCAAAAGATCCAGCTCATACCTACATCAG 4028
 Db 263 TTGCTTCATCATATTCGTGACAGACCTGACCAAAAGATCCAGCTCATACCTACATCAG 204
 Db 4029 ACAAAATATGCGCGTGTCTCTGTATCAAACTATTTGGTTTGGTTTGGAAACGCC 4088
 Db 203 ACAAAATATGCGCGTGTCTCTGTATCAAACTATTTGGTTTGGTTTGGAAACGCC 144
 Db 4089 ACGTACTTGGCATACCGCTGCAAGAGATGCAATGCAATGCAATGCAATGCAATGCAAT 4148
 Db 143 ACTGACTTGGCATACCGCTGCAAGAGATGCAATGCAATGCAATGCAATGCAATGCAAT 84
 Db 4149 AATTGGAAGAAAGATTATTAATTAACCGTATATTTTATACGACAAATTAATGTTTCT 4208
 Db 83 AATTGGAAGAAAGATTATTAATTAACCGTATATTTTATACGACAAATTAATGTTTCT 24
 Db 4209 ACAGATTTTATTTTATACAGAC 4231
 Db 23 ACAGATTTTATTTTATACAGAC 1

RESULT 7
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 LOCUS A1436212.1 Source: NIH/NCBI, GeneBank, CDNA clone, IMAGE:2124824
 DEFINITION 3' similar to gp.M87720. Fibroblast Growth Factor Receptor 2
 ACCESSION A1436212.1 GI:4308606
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens.
 CHORDATA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 755)
 NCBI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Bethesda, MD 20892-0709
 This clone is available royalty-free through LNC. Contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
 Insert Length: 895 Std Error: 1.00
 Seq primer: -400bp from Glibco
 High quality sequence stop: 443.
 FEATURES
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="IMAGE:2124824"
 /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
 /lab_protocol="108"
 /protocol="see below"
 (Pharmacia) with a modified polylinker. Site 1: Not 1; Site 2: Eco RI. Equal amounts of plasmid DNA from three normalised libraries (melanocyte 2NDH9, pregnant uterus NBH9U, and fetal heart NBH19N) were mixed, and six circles were used in vitro. Following NAR purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 500 cells each from the same 60232-26522.
 340488-345479, and 484488-489479.
 139 c 147 g 216 t 1 others

Query Match 16.1% Score 686.8; Db 9; Length 755;
 Best Local Similarity 96.0%; Pred. No. 3; 7e-135.

Matches 725; Conservative 0; Mismatches 28; Indels 2; Gaps 2;
 Db 3439 ACTAGTAAATCATTTTGGTGGACTTAAGTATATGACATCTCTTGAAGAGATATT 3498
 Db 755 ACTAGTAAATCATTTTGGTGGACTTAAGTATATGACATCTCTTGAAGAGATATT 696
 Db 3499 ACAATATATGACAAATTTGGGAAAAGAAAGATTTGATTTATTTGGTTTAAATCTGCT 3558
 Db 695 ACAATATATGACAAATTTGGGAAAAGAAAGATTTGATTTATTTGGTTTAAATGCTG 636
 Db 3559 GTGACACATTTGTTTACGCTCTTAATGCTCCATTAAGACATTAAGACATTAAGAC 3618
 Db 635 GTGACACATTTGTTTACGCTCTTAATGCTCCATTAAGACATTAAGACATTAAGAC 576
 Db 3619 ACGTGTTCATTTTGTGTGCAACCGCTCATTTACGTCACGACGATCTGATGACTT 3678
 Db 575 ACGTGTTCATTTTGTGTGCAACCGCTCATTTACGTCACGACGATCTGATGACTT 516
 Db 3679 CCCAATTAATTTGTTACGACGCTCTCTTAAAGATGCTTTAATCCTTCTTGAGACA 3738
 Db 515 CCCAATTAATTTGTTACGACGCTCTCTTAAAGATGCTTTAATCCTTCTTGAGACA 456
 Db 3739 GACCTTAGTGAATATGATAGCAATATGCTGCTCTCTGACGCTGCTCTCTG 3798
 Db 455 GACCTTAGTGAATATGATAGCAATATGCTGCTCTCTGACGCTGCTCTCTG 396
 Db 3799 ACGTGCACATTAATGATATGACCTGCTGATCTCTCTGATGATATTTGATATGCTTCA 3857
 Db 395 ACGTGCACATTAATGATATGACCTGCTGATCTCTCTGATGATATTTGATATGCTTCA 336
 Db 3858 GACCTCTTT-GCGTGTGAGACGCTGTAGAGATCTTCAGTGCATGATGAAATTTGAA 3916
 Db 335 GACCTCTTTGCGGTGAGACGCTGTAGAGATCTTCAGTGCATGATGAAATTTGAA 276
 Db 3917 CACAGACTTGTCTCTGATAGTTTGTGAGATAGCTCATCTTTTAAAGATCTCTTTC 3976
 Db 275 CACAGACTTGTCTCTGATAGTTTGTGAGATAGCTCATCTTTTAAAGATCTCTTTC 216
 Db 3977 ATCTAATTTCTGGACGACCTGACCAAAAGATGCTGATACCTGATGACCAAAATTA 4036
 Db 215 ATCTAATTTCTGGACGACCTGACCAAAAGATGCTGATACCTGATGACCAAAATTA 156
 Db 4037 TGGCGCTGCTCTCTGATAGTTTGTGAGATAGCTCATCTTTTAAAGATCTCTTTC 4096
 Db 155 TGGCGCTGCTCTCTGATAGTTTGTGAGATAGCTCATCTTTTAAAGATCTCTTTC 96
 Db 4097 TGCATAATGCTGACGATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 4156
 Db 95 TGCATAATGCTGACGATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 36
 Db 4157 AAAGTATTTTAAAGCTGTTTATTTTATCTG 4191
 Db 35 AAAGTATTTTAAAGCTGTTTATTTTATCTG 1

RESULT 8
 BM792391 693 bp mRNA linear EST 05-MAR-2002
 LOCUS BM792391.1 Source: NIH/NCBI, GeneBank, CDNA clone, S22SNU016n1, 28-B10
 DEFINITION 5' mRNA sequence.
 ACCESSION BM792391
 VERSION BM792391.1 GI:19140623
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens.
 CHORDATA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 693)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Kim, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)


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Db 698 CTTAAAGCCCCATATTAAAA..ACTGATTTATAGACAGGCTGTCATTTGCGTGTCAC 640
Oy 3643 CTTCTCATACGTACACGACACGTCTAACTGATGCTCCCAAGTAATAGATCCAGGCTC 3702
Db 639 CTTCTCATACGTACACGACACGTCTAACTGATGCTCCCAAGTAATAGATCCAGGCTC 580
Oy 3703 CTTCTTAAGAATCCCTTAATATCATCTCTGACAGACAGCTAGTGTAAATGATACAGCA 3762
Db 579 CTTCTTAAGAATCCCTTAATATCATCTCTGACAGACAGCTAGTGTAAATGATACAGCA 520
Oy 3763 ATCTGCTCTCTCTCTGACAGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3822
Db 519 ATCTGCTCTCTCTCTGACAGACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 460
Oy 3823 TG-ATGCTCTCTCTCTGAGTAATTTGATATAGCTGCTCAGACACTCTT-AGCTGAGAGAGCTC 3880
Db 459 TGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 400
Oy 3881 CTTTACATCTCTCAATCCCATCATACAAAATTTGAACACAGAGTGTCTCTCTCATCTT 3940
Db 399 CTTTACATCTCTCAATCCCATCATACAAAATTTGAACACAGAGTGTCTCTCTCATCTT 340
Oy 3941 TTGGGATAGTCCATCATCTTTTAAAGGATTTGCTTATCTATTGTGGAGACAGCTCCAC 4000
Db 339 TTGGGATAGTCCATCATCTTTTAAAGGATTTGCTTATCTATTGTGGAGACAGCTCCAC 280
Oy 4001 AAAACATGACGCTGATACCTACTACATGACAAAATATGCGCTGCTCTCTCTCTACTAA 4060
Db 279 AAAACATGACGCTGATACCTACTACATGACAAAATATGCGCTGCTCTCTCTCTACTAA 220
Oy 4061 ACTATGCTGTTTGTCTTTGGAAACACCATGCTACTTTGCACTACCGCTGCAAGATGATC 4120
Db 219 AGTATGCTGTTTGTCTTTGGAAACACCATGCTACTTTGCACTACCGCTGCAAGATGATC 160
Oy 4121 CAGATTAAGTACGATCTGATGTTTGAATGAGAAATGAGAAATGATTAATTAATTAAT 4180
Db 159 CAGATTAAGTACGATCTGATGTTTGAATGAGAAATGAGAAATGATTAATTAATTAAT 100
Oy 4181 TTTTATTAAGTACATTAATAATGTTTCTTAAGATTTTAATGTAACAGCAATAATTAAT 4240
Db 99 TTTTATTAAGTACATTAATAATGTTTCTTAAGATTTTAATGTAACAGCAATAATTAAT 40
Oy 4241 GTCCGCACTTAAAAAATTTTTAAAAA 4268
Db 39 GTCCGCACTTAAAAAATTTTTAAAAA 12

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FEATURES
Source
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetic Information: The following repetitive elements were found in this cDNA
sequence: 1-46, >AT-richlow.complexity (matched complement)
216-266, >(TA)nSimple_repeat
Seq primer: M13 FORWARD
POLY(A)-yes.
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-abu-b-07-0-UI"
/clone_type="UI-CF-EC1"
/tissue_type="lung"
/db_xref="DB010 (Life Technologies) (T1 phage resistant)"
/notes="Origin: Lung; Vector: pTZ19 (Life Technologies) with a
multiple cloning site (MCS) at position 1122. The cDNA library
UI-CF-EC1 is a normalized cDNA library containing the following
tissues(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
3' poly(A) tail. The oligo-dT primer was annealed to the
adaptor digested with Not I and cloned directionally
into pTZ19-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(art)18 tail. The sequence tag for this library is
AGCTGCTTAC-CF-EC1
TNG-TISSUE=Non-mal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TNG-SBO=AGCTGCTTAC"
BASE COUNT 210 a 136 c 120 g 224 t
ORIGIN
Query Match 15 83; Score 675; DB 14; Length 690;
Best Local Similarity 99.38; Pval No 1.2e-112;
Matches 678; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 2700 TCTCTAGTATCCACATTAAGGCGAGGTGTAAACATGATAGTCTGTCGCTGCTCC 2759
Db 690 TCTCTAGTATCCACATTAAGGCGAGGTGTAAACATGATAGTCTGTCGCTGCTCC 631
Oy 2760 CCAAAAGGACAGACATGAGACCTGATAGCTGTAAAGACATGATAGTCTGTCGCTCC 2819
Db 630 CCAAAAGGACAGACATGAGACCTGATAGCTGTAAAGACATGATAGTCTGTCGCTCC 571
Oy 2820 CTTGTGTCTCCATCTTATATATGATGACAGAGAGCTTAATATTTGAAAGATACAGC 2879
Db 570 CTTGTGTCTCCATCTTATATATGATGACAGAGAGCTTAATATTTGAAAGATACAGC 511
Oy 2880 AATATGCTTAAAGTTTATACATTTGAAATCTGTCGCTCCAGAGAGAAAGCT 2939
Db 510 AATATGCTTAAAGTTTATACATTTGAAATCTGTCGCTCCAGAGAGAAAGCT 451
Oy 2940 TTCTGAGACAGTGAAGCAGACAGCAAGCTACCCCTGACAGCTCCGCTGCTTCT 2999
Db 450 TTCTGAGACAGTGAAGCAGACAGCAAGCTACCCCTGACAGCTCCGCTGCTTCT 391
Oy 3000 GCGTGTGACAGTGAAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGAC 3059
Db 390 GCGTGTGACAGTGAAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGAC 331
Oy 3060 ATTAATGAGAAATTTATGTCACAGCACTTACAGAGCAGCAATATCAGATATAGATG 3119
Db 330 ATTAATGAGAAATTTATGTCACAGCACTTACAGAGCAGCAATATCAGATATAGATG 271

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[illegible][illegible]

Qy	3219	CGGAAATGCGCCTCTTTTAACTATGCTGTAATGTCCTGACATA	3278
Qy	3220	CGGAAATGCGCCTCTTTTAACTATGCTGTAATGTCCTGACATA	3279
Db	121	CGTAAATATGTCCTCTTTTAACTATGCTGTAATGTCCTGACATA	180
Qy	3279	ATTCTTAATTTTACGACACGAGGTGGAAAAATCTTTTGGCTTCAGGAAAAATGGCT	3338
Db	181	ATTCTTAATTTTACGACACGAGGTGGAAAAATCTTTTGGCTTCAGGAAAAATGGCT	240
Qy	3339	TACCTTAATTTTAAATATGTTATATACAAAACATTAATCACTTATAGTTTTT	3398
Db	241	TACCTTAATTTTAAATATGTTATATACAAAACATTAATCACTTATAGTTTTT	300
Qy	3399	TTCGTAATTAATGCGAATTTCTATGACGCGACACACGACATGATCATATAGTCTCTG	3458
Db	301	TTCGTAATTAATGCGAATTTCTATGACGCGACACACGACATGATCATATAGTCTCTG	360
Qy	3459	GACCTTAACGTATACATCTCTTGGAAAAAGAAATTTTACATATAGTAAATTTGG	3518
Db	361	GACCTTAACGTATACATCTCTTGGAAAAAGAAATTTTACATATAGTAAATTTGG	420
Qy	3519	GGAATTAAGTTTAAATTTATGTTTAAAGTCGCTGACAGATCTGTTCTAGA	3578
Db	421	GGAATTAAGTTTAAATTTATGTTTAAAGTCGCTGACAGATCTGTTCTAGA	480
Qy	3579	CGTCCTAATGCGCCATTTAAAGAAACATCAATGAGAGGGTTCACTTTGGTGTG	3638
Db	481	CGTCCTAATGCGCCATTTAAAGAAACATCAATGAGAGGGTTCACTTTGGTGTG	540
Qy	3639	CACCGGTGATTAAGGTAAACGCAACGTCTAACTGACTCCGAGATAAATGGTACAG	3698
Db	541	CACCGGTGATTAAGGTAAACGCAACGTCTAACTGACTCCGAGATAAATGGTACAG	600
Qy	3699	CGACCTCTTAATATGCTCAACGACAGCGTCTAACTGAGCAAGCTAGTAAATGATAG	3758
Db	601	CGACCTCTTAATATGCTCAACGACAGCGTCTAACTGAGCAAGCTAGTAAATGATAG	660
Qy	3759	CAGATATGGTTCTTCGCGACGCTGCGCTTCGCTTGGAGTTGCA	3805
Db	661	CAGATATGGTTCTTCGCGACGCTGCGCTTCGCTTGGAGTTGCA	707

	RESULT 12		
BQ757816/c			
DEFINITION	593 bp cDNA	mRNA	EEST_19-JUN-2002
ACCESSION	U01-H-E22	-bbh-g-11-o-UI st NCBI CGAP m23 homo sapiens cDNA clone	
VERSION	UI-H-E22	-bbh-g-11-o-UI st , mRNA sequence.	
KEYWORDS	BQ757816		
SOURCE	BQ757816.1	GI:21479133	
ORGANISM	human,		
	human sapiens		
	Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Dumetia; Plestitia; Primates; Charitini; Homnidae; Homo.		
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/hicgap.		
AUTHORS	1 (bases 1 to 693)		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).		
JOURNAL	Tumor Gene Index		
COMMENT	(Unpublished) (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: sgap@remail.nih.gov		
	Contractor: Dr. Steven Altalis/ Rush Presbyterien, Dept. of Orthopedics		
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, university of Iowa		
	Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu		
	The following repetitive elements were found in this cDNA sequence:		
	217-267, >(TA)n(n=1-6), complexity (matched complement)		
	Seq primer: M13 FORWARD		
	POLYA-Tes.		

Db	181	GCACAGAGTACCAACCCATCCCTCCCTGGGAGACAGGTATACAGTTGGCCGAGTCCG	240
Qy	1578	CTCTCTCTGAGAACTTCCACACCCCGCTGGGTGATGTAAACACACGCTCTCTTCCACAGCC	1637
Db	241	CTCTCTCTGAACTCCACACCCGCTGGGTGATGTAAACACGCTCTCTTCCACAGCC	300
Qy	1638	AGACACCCCATCTGCTGGCAGGGGCTCCGAGTATGACATCTCCAGACGCCCAAAATGSGA	1697
Db	301	GAACACCCCATCTGCTGGCAGGGGCTCCGAGTATGACATCTCCAGACGCCCAAAATGSGA	360
Qy	1598	CTTTCACAGAGTATGAGCTGACATGGGCAACACCCCTGGGACAGCTGCTTTGGGCAAGT	1757
Db	361	ATTTCCTCCAGAGTATGAGCTGACATGGGCAACACCCCTGGGAGAAAGTTCTTTGGGCAAGT	420
Qy	1758	GCTCATGTGGCGGACACAGTGGGAAATTGGCAAAAGACCAACCCCAAGGAGCGGGTACCCGTGC	1817
Db	421	AGCTATGTGGCGGACACAGTGGGAAATTGGCAAAAGACCAACCCCAAGGAGCGGGTACCCGTGC	480
Qy	1818	CTTTCAGAGTGTGGAACAGAGATGGCACAGAGAAAGACCTTTCTGATCTGGGTGTACAGA	1876
Db	481	AGTGAAGTGTGGAAGATGATATGTCACAGAGAGAGATCTGTCTATCTGTGTATCAAGAA	540
Qy	1877	TGGAGATGATGAAGATGATTTGGGAAACAAAGAAATATCTTTCTTTGGACCTGCGA	1936
Db	541	TGGAGATGATGAAGATGATTTGGGAAACAAAGAAATATCTTTCTTTGGACCTGCGA	600
Qy	1937	CACAGATATGGGCTCTCTCTCTATGCTATGATGATGCTGCTTAAAGCAACCTCCGAGAAAT	1996
Db	601	CGGAGATATGGACCTCTCTCTCTATGCTATGATGATGCTGCTTAAAGCAACCTCCGAGAAAT	660
Qy	1997	ACCTCGAGACCCGACAGGCGACCGGATGAGAGTACCTATGAGATATTAACCTGCTTCTCT	2055
Db	661	ACCTCGAGACCCGACAGGCGACCGGATGAGAGTACCTATGAGATATTAACCTGCTTCTCT	719
Qy	2056	GAGGACAGACAGATCT	2115
Db	720	GAGGACAGACAGATCT	779
Qy	2116	CAGTACTTGGCTCTCCCAAAATGATATTCATGATGAGATTATAGCAGCGCAAAATCTTTGGTA	2175
Db	780	CAGTACTTGGCTCTCCCAAAATGATATTCATGATGAGATTATAGCAGCGCAAAATCTTTGGTA	839
Qy	2176	ACGAAAGCA 2186	
Db	840	ACGAAAGCA 850	
RESULT 14			
BI661662			
LOCUS	BI661662	787 bp	mRNA
DEFINITION	Mus musculus NCL clone IMAGE:5351304 5'		
ACCESSION	BI661662.1		EST 12-SEP-2001
VERSION	BI661662.1		GI:15575898
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryote, Metazoa: Chordata, Craniata: Vertebrata: Euteleostomi;		
AUTHORS	1 (base), Eberhard, Roderick L, Schlumpacher, Muriel; Murine, Mus.		
TITLE	N1H-MGC http://imgc.ncl.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cegapb@ncl.nih.gov		
	Tissue Procurement: Lohrer Hemmighausen Ph.D., Priscilla Purth		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		

FEATURES	source	organism="Mus musculus"	strain="NHRI"	db_xref="taxon:10090"	clone="IMAGE:5351304"	clone_lib="NCI_COAP_Mind"	tissue_type="tumor, gross tissue"	dev_stage="5 months"	lab_host="DHIOs"	vector="PCMV-SpOBF5, Site.1: S&11; Site.2: NotI; Cloned unidirectionally. Primer:oligos library constructed by Life Technologies, investigators: Klaus Hemminger/Piscicella Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1995)."
BASE COUNT	223	a	176	c	221	g	167	t		
Query Match	15.6%	Score 664;	DB 13;	Length 787;						
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Db	241	TAGAGATATATATCAACCTCTGAGAGCGCGACACAGATGAGGCGCTCTCATGTCTATAGT	300							
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Db	301	TGAAATGCTCTTAAAGAGACCTCTCGGGAATCTCCGAGCGCGAGAGCGCACCCGTCAT	360							
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Qy	2325	TGATGATGCTGCTCGGAGGTATATATGATGAGAGATCTTTTGAATATATATATATATATAT	2384							
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 Oy 2445 GCGAGCA 2452
 Db 780 GCGAGCA 787
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 mRNA sequence.
 ACCESSION B1853362
 VERSION B1853362.1 GI:15994109
 KEYWORDS EST.
 SOURCE House mouse.
 ORGANISM Mus musculus.
 COMMENT
 Reference: 1 (bases 1 to 852)
 NIH-MGC http://mgi.mc.man.ac.uk/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Tissue Procurement: Lotter Hemmighausen Ph.D., Priscilla Furch
 Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution. Information can be
 found at: <http://imgc.llnl.gov>
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 Location/Qualifiers
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 /clone="IMAGE:5587938"
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 /tissue_type="tumor, gross tissue"
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 /note="Organ: mammary; Vector: pCMV-Sport6; Site:1; Salt:
 size: 852; Nucleic acid: cDNA; Directionality: 5' to 3';
 Providing samples: Lotter Hemmighausen/Priscilla Furch
 NIH Reference for transgenic model: Li et al., Cell Growth
 and Differentiation 7, 3-11 (1996)."
 BASE COUNT 231 a 218 c 203 g 200 t
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 Identical 90.08; Pct Ident 76.78; Indels 7; Gaps 5;
 Mismatches 767; Conservative 0; Mismatches 78;
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 Oy 2059 GAGCAGATGACCTTCAAGGACTGTGTCTACCTACCTACGAGCGAGAGCTGAGAG 2118
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 Db 241 ACAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
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 Db 301 CTATTACAAAAGACACAAATGAGGAGGCTCTCGAGTCAAGTGGCTCCAGAACGCT 360
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 Db 361 TTTTGGATGAGATTACATCATGACAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Oy 2358 GATCTTCACTTTAGGAGGAGGCTGCGCTGACCCAGGAGATTTCCGCTGAGGAACTTTTAAGCT 2417
 Db 421 GATCTTCACTTTAGGAGGAGGCTGCGCTGACCCAGGAGATTTCCGCTGAGGAACTTTTAAGCT 480
 Oy 2418 GCTCAAGACAGTACGAGGAGGCTGCGCTGACCCAGGAGATTTCCGCTGAGGAACTTTTAAGCT 480
 Db 481 GCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 Oy 2478 GATGAGGAGCTGTGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2537
 Db 541 GATGAGGAGTGTGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Oy 2538 AGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2597
 Db 601 AGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
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 Db 721 TTCTGTGTTTCTGCTGCAAGCCGATGCTTAAAGAACATGCTTGTGCTGATGATGACAC 780
 Oy 2716 ATAAAGCGAGTGTAAAGCATGATG-CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2771
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 Oy 2772 GCACTGGGAGAC 2783
 Db 841 GCACTGGGAGAC 852

Search completed: December 11, 2002, 17:35:12
 Job time: 3758 secs

GenCore version 5.1.3
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OK nucleic - nucleic search, using SW model

Run on: December 11, 2002, 17:40:42; Search time 120 Seconds

(Without alignments)
13668,608 Million cell updates/sec

Title: US-09-954-556-3

Sequence score: 4268 1 cccaagaccacattcttcgc.....acttaaaaaaaaaaaaaa 4266

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 189974

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24.2	0.6	31	10	US-09-801-274-958 Sequence 958, App
2	23.4	0.5	36	10	US-09-827-289-25 Sequence 957, App
3	22.6	0.5	50	10	US-09-815-241-1012 Sequence 957, App
4	22.4	0.5	50	10	US-09-827-289-21 Sequence 22, Appl
5	22.4	0.5	46	10	US-09-827-289-22 Sequence 22, Appl
6	22.2	0.5	46	10	US-09-827-289-22 Sequence 22, Appl
7	21.8	0.5	46	10	US-09-827-289-24 Sequence 13, Appl
8	21.8	0.5	46	10	US-09-827-289-24 Sequence 24, Appl
9	21.8	0.5	48	9	US-09-864-785-3604 Sequence 3604, Ap
10	21.8	0.5	48	9	US-09-827-289-26 Sequence 26, Appl
11	21.4	0.5	46	10	US-09-827-289-24 Sequence 20, Appl
12	21.4	0.5	46	10	US-09-827-289-24 Sequence 20, Appl
13	21.2	0.5	35	9	US-09-827-777A-72 Sequence 5, Appl
14	20.8	0.5	42	10	US-10-023-096-5 Sequence 2, Appl
15	20.8	0.5	42	10	US-09-828-592-2 Sequence 20, Appl
16	20.8	0.5	46	10	US-09-827-289-20 Sequence 30, Appl
17	20.6	0.5	46	10	US-09-864-785-3455 Sequence 1, Appl
18	20.6	0.5	44	10	US-10-023-293-30 Sequence 30, Appl
19	20.6	0.5	45	12	US-10-023-293-30 Sequence 30, Appl

20	20.6	0.5	48	9	US-09-864-785-3333 Sequence 3333, Ap
21	20.6	0.5	48	9	US-09-864-785-3472 Sequence 3472, Ap
22	20.6	0.5	48	9	US-09-864-785-3501 Sequence 3501, Ap
23	20.2	0.5	32	10	US-09-865-807-32 Sequence 32, Appl
24	20.2	0.5	37	9	US-09-864-785-3378 Sequence 3378, Ap
25	20.2	0.5	37	9	US-09-864-785-3378 Sequence 3378, Ap
26	20.2	0.5	48	9	US-09-864-785-3378 Sequence 68, Appl
27	20.2	0.5	48	10	US-09-732-914-73 Sequence 73, Appl
28	20.2	0.5	48	10	US-09-732-914-73 Sequence 80, Appl
29	20.2	0.5	48	10	US-09-732-914-80 Sequence 4, Appl
30	20	0.5	20	10	US-09-073-881-4 Sequence 24, Appl
31	20	0.5	22	10	US-09-073-881-24 Sequence 26, Appl
32	19.8	0.5	40	10	US-09-245-802-45 Sequence 12, Appl
33	19.8	0.5	40	10	US-09-827-289-12 Sequence 16, Appl
34	19.8	0.5	45	10	US-09-827-289-12 Sequence 21, Appl
35	19.8	0.5	45	10	US-09-827-289-12 Sequence 21, Appl
36	19.8	0.5	46	10	US-09-827-289-25 Sequence 3109, Ap
37	19.8	0.5	48	9	US-09-864-785-3109 Sequence 3109, Ap
38	19.8	0.5	48	9	US-09-864-785-3338 Sequence 3338, Ap
39	19.8	0.5	48	9	US-09-864-785-3338 Sequence 3338, Ap
40	19.8	0.5	48	9	US-09-864-785-3455 Sequence 1, Appl
41	19.8	0.5	35	9	US-10-034-451-1 Sequence 9, Appl
42	19.6	0.5	36	9	US-09-590-932A-99 Sequence 9, Appl
43	19.6	0.5	36	9	US-10-047-593-6 Sequence 6, Appl
44	19.6	0.5	36	9	US-10-090-035-25 Sequence 25, Appl
45	19.6	0.5	36	9	US-10-090-035-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-801-274-958
Sequence 958, Application US/09801274
Genet. No. 20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michèle
APPLICANT: Ireland, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825, 2009-001
CURRENT APPLICATION NUMBER: US/09/801, 274
PRIORITY APPLICATION NUMBER: US/01/60/187, 510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206, 129
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FASTSD for Windows Version 4.0
SEQ ID NO 958
GENET. NO. 20020032319A1
TYPER DNA
ORGANISM: Homo sapiens
US-09-801-274-958
Query Match 0.6%; Score 24.2; DB 10;
Best Local Similarity 83.9%; Pred. No. 7.8e+03;
Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1034 ACCGCCCATCTTCGACGCGGCGGCGTCCGCGC 31
DB 1 ACCGCCCATCTTCGACGCGGCGGCGTCCGCGC 31
RESULT 2
US-09-827-289-25/c
Sequence 25, Application US/09827289
Genet. No. US20020009716A1
GENERAL INFORMATION:
APPLICANT: Abarrua, Patricia
TITLE OF INVENTION: Process for Allele Discrimination using Primer
FILE REFERENCE: 469290-55

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? CURRENT APPLICATION NUMBER: US/09/827.289
? PRIOR FILING DATE: 2001-04-05
? PRIOR APPLICATION NUMBER: U.S. 60/194843
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 25
? LENGTH: 46
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE INFORMATION: Description of Artificial Sequence: P1 primer for
? OTHER INFORMATION: use in allele discrimination
US-09-827-289-25

Query Match 0.5% Score 23.4; DB 10; Length 46;
Best Local Similarity 73.2%; Pred. No. 1.5e+04;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

? 4228 AGCGAATAAATGTCACGCACCTTAATAAAAAAAAAAAAAA 4268
? DB 46 AGCGAATAAATGTCACGCACCTTAATAAAAAAAAAAAAAA 6

RESULT 3
US-09-801-274-957
? Sequence 357, Application US/09801274
? Patent No. US20020032319A1
? GENERAL INFORMATION:
? APPLICANT: Cargill, Michele
? APPLICANT: Ireland, James S.
? TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
? FILE REFERENCE: 2023-2009-001
? CURRENT FILING DATE: 2001-03-07
? PRIOR FILING DATE: 2000-03-07
? PRIOR APPLICATION NUMBER: US 60/187.510
? PRIOR FILING DATE: 2000-05-22
? NUMBER OF SEQ ID NOS: 1802
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 957
? LENGTH: 31
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-801-274-957

Query Match 0.5% Score 22.6; DB 10; Length 31;
Best Local Similarity 80.4%; Pred. No. 1.5e+04;
Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

? 2453 ACTGCACACGACGACGTGATGATGATGACG 2483
? DB 1 ACTGCACACGACGACGTGATGATGATGACG 31

RESULT 4
US-09-815-343-1012/C
? Sequence 1012, Application US/0981543
? Patent No. US20010055596A1
? GENERAL INFORMATION:
? APPLICANT: Mesinger, Madeline
? APPLICANT: Xu, Jiangchun
? TITLE OF INVENTION: METHODS AND PROCEDURES FOR THERAPY AND
? TITLE OF INVENTION: DIAGNOSIS OF COLOR CANCER
? FILE REFERENCE: 210.21.504
? CURRENT APPLICATION NUMBER: US/09/815.343
? CURRENT FILING DATE: 2001-03-22
? NUMBER OF SEQ ID NOS: 1556
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1012
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? LENGTH: 50
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-815-343-1012

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Best Local Similarity 68.9%; Pred. No. 2.3e+04;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

? 4224 AACAGACAAATTAATGTCACGCACCTTAATAAAAAAAAAA 4268
? DB 47 AACAGACAAATTAATGTCACGCACCTTAATAAAAAAAAAA 3

RESULT 5
US-09-827-289-21/C
? Sequence 21, Application US/09827289
? Patent No. US2002009716A1
? GENERAL INFORMATION:
? APPLICANT: Process for Allele Discrimination Using Primer
? TITLE OF INVENTION: Extension
? FILE REFERENCE: 469290-55
? CURRENT APPLICATION NUMBER: US/09/827.289
? CURRENT FILING DATE: 2001-04-05
? PRIOR APPLICATION NUMBER: U.S. 60/194843
? PRIOR FILING DATE: 2000-04-05
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 21
? LENGTH: 46
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE INFORMATION: Description of Artificial Sequence: P1 primer for
? OTHER INFORMATION: use in allele discrimination
US-09-827-289-21

Query Match 0.5% Score 22.4; DB 10; Length 46;
Best Local Similarity 72.5%; Pred. No. 2.5e+04;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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? DB 45 GCGAATTAATGTCACGCACCTTAATAAAAAAAAAAAAAA 6

RESULT 6
US-09-827-289-22/C
? Sequence 22, Application US/09827289
? Patent No. US2002009716A1
? GENERAL INFORMATION:
? APPLICANT: Abazura, Patricia
? TITLE OF INVENTION: Process for Allele Discrimination Using Primer
? FILE REFERENCE: 469290-55
? CURRENT APPLICATION NUMBER: US/09/827.289
? CURRENT FILING DATE: 2001-04-05
? PRIOR APPLICATION NUMBER: U.S. 60/194843
? PRIOR FILING DATE: 2000-04-05
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 22
? LENGTH: 46
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE INFORMATION: Description of Artificial Sequence: P1 primer for
? OTHER INFORMATION: use in allele discrimination
US-09-827-289-22

Query Match 0.5% Score 22; DB 10; Length 46;
Best Local Similarity 67.4%; Pred. No. 3.1e+04;
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Matches 31: Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 4223 TACAGCAAAATTAATGTACGCACTTAAAAA 4268
 DB 46 TACAGCAAAATTAATGTACGCACTTAAAAA 4268

RESULT 7
 US-09-875-5194-13/c
 Sequence 13: Application US/09875519A

Patent No. US20020068059A1
 GENERAL INFORMATION:
 APPLICANT: Harrison, Timothy C.
 APPLICANT: Parfies, Richard A.
 TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
 FILE REFERENCE: 4-30443/A/INT/PCF
 CURRENT APPLICATION NUMBER: US/09/875,519A
 PRIOR FILING DATE: 2001-08-06
 CURRENT FILING DATE: 2001-08-06
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 13
 LENGTH: 44
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-875-5194-13

Query Match
 Best Local Similarity 70.7%; Pred. No. 3,4e+04;
 Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1866 GGTGTCAAGATGAGATGATGAGATGCGGAACCA 1906
 DB 41 GGTGTCAAGATGAGATGATGAGATGCGGAACCA 1

RESULT 8
 US-09-827-289-24/c
 Sequence 24: Application US/09827289
 Patent No. US2002009716A1
 GENERAL INFORMATION:
 APPLICANT: Ahrens, Patricia
 TITLE OF INVENTION: Process for Allele Discrimination Using Primer
 FILE REFERENCE: 469290-55
 CURRENT APPLICATION NUMBER: US/09/827,289
 PRIOR APPLICATION DATE: 2001-04-05
 PRIOR FILING DATE: 2000-04-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 24
 LENGTH: 46
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: P1 primer for
 OTHER INFORMATION: use in allele discrimination
 US-09-827-289-24

Query Match
 Best Local Similarity 70.7%; Pred. No. 3,4e+04;
 Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 4228 AGACAAATTAATGTACGCACTTAAAAA 4268
 DB 46 AGACAAATTAATGTACGCACTTAAAAA 4268

RESULT 9
 US-09-864-785-3604
 Sequence 3604: Application US/09864785

Patent No. US20020177568A1
 GENERAL INFORMATION:
 APPLICANT: Rhozyme Pharmaceuticals, Inc.
 APPLICANT: Stinchcomb, Dan
 APPLICANT: Draper, Ken Jm
 APPLICANT: Kesseler, Jim

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
 FILE REFERENCE: 400/022 (MBH00-812-D)
 CURRENT APPLICATION NUMBER: US/09/864,785
 PRIOR FILING DATE: 2001-05-23
 CURRENT FILING DATE: 2001-05-23
 NUMBER OF SEQ ID NOS: 3929
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 3604
 LENGTH: 48
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: Nucleic Acid
 OTHER INFORMATION: use in allele discrimination
 US-09-864-785-3604

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 Best Local Similarity 60.6%; Pred. No. 3,5e+04;
 Matches 20; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 2052 TCTTAGAGCGCATGACCTTCAGCACTGCG 2084
 DB 3 TCTTAGAGCGCATGACCTTCAGCACTGCG 35

RESULT 10
 US-09-827-289-26/c
 Sequence 26: Application US/09827289
 Patent No. US2002009716A1
 GENERAL INFORMATION:
 APPLICANT: Ahrens, Patricia
 TITLE OF INVENTION: Process for Allele Discrimination Using Primer
 FILE REFERENCE: 469290-55
 CURRENT APPLICATION NUMBER: US/09/827,289
 PRIOR APPLICATION DATE: 2001-04-05
 PRIOR FILING DATE: 2000-04-05
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 26
 LENGTH: 46
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: P1 primer for
 OTHER INFORMATION: use in allele discrimination
 US-09-827-289-26

Query Match
 Best Local Similarity 68.2%; Pred. No. 3,8e+04;
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 4225 ACAGCAAAATTAATGTACGCACTTAAAAA 4268
 DB 44 ACAGCAAAATTAATGTACGCACTTAAAAA 4268

RESULT 11
 US-09-827-289-20
 Sequence 20: Application US/09827289
 Patent No. US2002009716A1
 GENERAL INFORMATION:
 APPLICANT: Ahrens, Patricia
 TITLE OF INVENTION: Process for Allele Discrimination Using Primer
 FILE REFERENCE: 469290-55
 CURRENT APPLICATION NUMBER: US/09/827,289

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? CURRENT FILING DATE: 2001-04-05
? PRIOR APPLICATION NUMBER: U.S. 60/194843
? PRIOR FILING DATE: 2000-04-05
? INVENTOR: US/020172953A1
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 20
? LENGTH: 46
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE: ORIGIN: Description of Artificial Sequence: Pl primer for
? OTHER INFORMATION: use in allele discrimination
US-09-827-289-20

Query Match
Best Local Similarity 0.5%; Score 21.4; DB 10; Length 46;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Cy 3386 TTTATAGCTTTTTCGTAATTAGGCAATTCATATGC 3424
DB 5 TTTTATTTTTCATTTTTCATTTTTCATTTTTCATTTTC 43

RESULT 12
US-09-827-289-24
Sequence 24: Application US/09827289
? Patent No. US20020059716A1
? INVENTOR: Kruzel, Marian L.
? APPLICANT: Aberrin, Patricia
? TITLE OF INVENTION: Process for Allele Discrimination Using Primer
? FILE REFERENCE: 469290-55
? CURRENT APPLICATION NUMBER: US/09/827,289
? PRIOR FILING DATE: 2001-04-05
? PRIOR APPLICATION NUMBER: 60/194843
? PRIOR FILING DATE: 2000-04-05
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 24
? LENGTH: 46
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE: ORIGIN: Description of Artificial Sequence: Pl primer for
? OTHER INFORMATION: use in allele discrimination
US-09-827-289-24

Query Match
Best Local Similarity 0.5%; Score 21.4; DB 10; Length 46;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Cy 3386 TTTATAGCTTTTTCGTAATTAGGCAATTCATATGC 3424
DB 5 TTTTATTTTTCATTTTTCATTTTTCATTTTTCATTTTC 43

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? CURRENT APPLICATION NUMBER: US/09/927,777A
? CURRENT FILING DATE: 2001-08-10
? PRIOR APPLICATION NUMBER: 09/820,279
? PRIOR FILING DATE: 2001-03-28/60,500
? PRIOR APPLICATION NUMBER: 60/224,631
? PRIOR FILING DATE: 2001-01-12
? PRIOR APPLICATION NUMBER: 09/603,830
? PRIOR FILING DATE: 2000-06-26
? PRIOR APPLICATION NUMBER: 09/344,667
? PRIOR FILING DATE: 1999-06-25
? PRIOR APPLICATION NUMBER: 09/240,795
? PRIOR FILING DATE: 1997-07-21
? PRIOR APPLICATION NUMBER: 60/031,809
? PRIOR FILING DATE: 1996-07-29
? PRIOR APPLICATION NUMBER: 60/176,409
? PRIOR FILING DATE: 2000-01-13
? PRIOR APPLICATION NUMBER: 60/192,699
? PRIOR FILING DATE: 2000-03-28/200,161
? PRIOR APPLICATION NUMBER: 60/213,906
? PRIOR FILING DATE: 2000-04-26
? PRIOR APPLICATION NUMBER: 2000-06-26
? PRIOR FILING DATE: 2000-08-11
? PRIOR APPLICATION NUMBER: 60/254,392
? PRIOR FILING DATE: 2000-12-08/255,235
? PRIOR APPLICATION NUMBER: 2000-12-11
? NUMBER OF SEQ ID NOS: 76
? SOFTWARE: Microsoft Word 2000
? SEQ ID NO 72
? LENGTH: 35
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE: ORIGIN: Description of Artificial Sequence: random
? OTHER INFORMATION: synthetic sequence
US-09-927-777A-72

Query Match
Best Local Similarity 0.5%; Score 21.2; DB 9; Length 35;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Cy 3166 AATATTACAGCACTATTTCGTCATGCAATTT 3199
DB 34 AATATTACAGCACTATTTCGTCATGCAATTT 1

RESULT 14
US-10-023-086-5/C
Sequence 5: Application US/10023096
? Patent No. US20020160941A1
? GENERAL INFORMATION:
? APPLICANT: Kruzel, Marian L.
? APPLICANT: Kurecki, Tomasz
? APPLICANT: Gollnick, Paul D.
? APPLICANT: Gollnick, Daniel J.
? TITLE OF INVENTION: Expression, and Uses of Human
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Jacobson, Price, Holman & Stern
? STREET: 400 Seventh St. N.W.
? CITY: Washington D.C.
? STATE: DISTRICT OF COLUMBIA
? ZIP: 20004
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/10/023,096
3
4 FILING DATE:
5 PRIORITY:
6 PRIOR APPLICATION DATA:
7 FILING DATE:
8 APPLICATION NUMBER: US/08/724,586
9 FILING DATE: 30-SEPT-1996
10 APPLICATION NUMBER: US 08/338,445
11 FILING DATE: 05-MAY-1994
12 APPLICATION NUMBER:
13 NAME: PLAYER, WILLIAM E.
14 REGISTRATION NUMBER: 31,409
15 REFERENCE/DOCKET NUMBER: 10505/P50185C
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 86.2023.638-6666
18 TELEFAX: 86.2023.638-6666
19 INFORMATION FOR SEQ ID NO: 5:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 42 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: single
24 ORIENTATION: 5' to 3'
25 MOLECULE TYPE: DNA (genomic)
26 HYPOTHEETICAL: NO
27 ANTI-SENSE: NO
28
29 US-10-023-096-5

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GenGene version 5.1.3
Copyright (c) 1995 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 17:35:24 (Search time 3671 Seconds)

(Without alignments)
18629.294 Million cell updates/sec

Title: US-09-954-556-3

Perfect score: 4268

Sequence: 1 cccaagaccctctctctgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:*

1: em.estba:*
2: em.estba:*
3: em.estba:*
4: em.estba:*
5: em.estba:*
6: em.estba:*
7: em.estba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	26.2	0.6	47	12	BF107886	BF107886 601823895
C 2	25.4	0.6	43	10	AV832677	AV832677 602823955
C 3	24.4	0.6	50	9	AA120437	AA120437 602823955
C 4	24.4	0.6	43	9	BF382680	BF382680 602823955
C 5	24.2	0.6	49	9	AA160945	AA160945 602823955
C 6	24.2	0.6	49	9	AA160945	AA160945 602823955

C 7	24.2	0.6	49	9	AA545635	AA545635 v165h05.r
C 8	24.2	0.6	50	9	AA500588	AA500588 A1500588
C 9	24.2	0.6	49	9	AA500588	AA500588 A1500588
C 10	23.8	0.6	45	9	AA58773	AA58773 A158773
C 11	23.8	0.6	45	9	AA58773	AA58773 A158773
C 12	23.8	0.6	45	12	BF691166	BF691166 602242757
C 13	23.8	0.6	45	12	BF691166	BF691166 602242757
C 14	23.8	0.6	50	9	AA107269	AA107269 A107269
C 15	23.8	0.6	50	9	AA107269	AA107269 A107269
C 16	23.6	0.6	46	2	HSN003158	HSN003158 HSN003158
C 17	23.6	0.6	46	2	HSN003158	HSN003158 HSN003158
C 18	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 19	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 20	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 21	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 22	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 23	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 24	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 25	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 26	23.2	0.5	45	9	AA590547	AA590547 A1590547
C 27	23.2	0.5	45	13	BF130882	BF130882 602981270
C 28	22.8	0.5	50	2	HSN002946	HSN002946 HSN002946
C 29	22.8	0.5	50	2	HSN002946	HSN002946 HSN002946
C 30	22.8	0.5	50	2	HSN002946	HSN002946 HSN002946
C 31	22.8	0.5	50	2	HSN002946	HSN002946 HSN002946
C 32	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 33	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 34	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 35	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 36	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 37	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 38	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 39	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 40	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 41	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 42	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 43	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 44	22.6	0.5	45	17	AA624922	AA624922 1M043619
C 45	22.6	0.5	45	17	AA624922	AA624922 1M043619

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

ATTACH

JOURNAL

COMMENT

FEATURES

BF107886 47 bp mRNA linear EST 19-OCT-2000
601823895R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043735 3'

LOCUS BF107886
DEFINITION mRNA sequence.
ACCESSION BF107886
VERSION BF107886.1 GI:10890412
KEYWORDS EST

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 47)
NIH_MGC http://mgi.ncl.nih.gov/
ATTACH PubMed 11599215
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@phs.fda.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
Cloning Distribution: The I.M.A.G.E. Consortium (LMU)
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHC866 row: n column: 24
High quality sequence start: 8
High quality sequence stop: 22.
Location/Qualifiers

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source
1. .47
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4043735"
/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: Placenta; Vector: pDNR-LIB (Clontech);
Site.1: SFI1 (ggccctctggcgc); Site.2: SFI1 (ggcattatggc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCGACGGCCAGCGCCGACATG-dT(30)BN-3'
(where B is A, C, G or T and N = A, C, G, or T). Average
length of the 3' adaptors is 18 bp. This library was
constructed from 1000 clones. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
Library."
BASE COUNT      5 a      1 c      3 g      38 t
ORIGIN
Query Match      0.68: Score 36.2: DB 12: Length 47:
Best Local Similarity 79.58: Pval: NO 6.5e-05:
Matches 31: Conservative 0: Mismatches 8: Indels 0: Gaps 0:

OY 4230 ACAATTAATGTCACCCACTTAATAAAAAAAAAA 4268
DB 46 AAAAAAAAAAATTAATTAACAAAAAAAAAAAAAAAAA 8

RESULT 2
LOCUS      AV832677      43 bp      mRNA      linear      EST 22-JUN-2001
DEFINITION AV832677 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgare top three leaves adult, heading stage Hordeum vulgare
vulgare subsp. vulgare cDNA clone baal1006, mRNA sequence.
ACCESSION  AV832677
VERSION     AV832677.1
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare.
ORGANISM    Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
Sato, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2001)
Contact: Kazuhito Sato
Research Institute for Resources
Genome and Environment, Barley Germplasm Center
Chuo 20-1, Shikida-cho, Japan 40046, Japan
Email: kazu@rib.okayama-u.ac.jp
URL: http://www.rib.okayama-u.ac.jp/barley/
Sato, K., Saitoh, D., Takeeda, K., Shint, T. and Kohara, Y. Direct
subcloning:
database: http://www.shigen.nig.ac.jp/barley/barley.html.
Location/Qualifiers
1 a
/organism="Hordeum vulgare subsp. vulgare"
/db_xref="taxon:112509"
/clone="baal1006"
/culture="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare top three leaves adult, heading
stage"
/dev_stage="adult"
/dev_stage="top three leaves"
/dev_stage="adult"
BASE COUNT      2 a      1 c      4 g      31 t      5 others
ORIGIN
Query Match      0.68: Score 25.4: DB 10: Length 43:
Best Local Similarity 72.58: Pval: NO 9.8e-05:
Matches 29: Conservative 0: Mismatches 11: Indels 0: Gaps 0:

```

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OY 4229 GACAAATTAATGTCACCCACTTAATAAAAAAAAAA 4268
DB 43 GACAAAAAAAAAATTAATTAACAAAAAAAAAAAAAAAAA 4

RESULT 3
LOCUS      AA120437      50 bp      mRNA      linear      EST 19-NOV-1996
DEFINITION AA120437 m47a11.f1 Beddington mouse embryonic region Mus musculus cDNA
clone IMAGE:541052 5', mRNA sequence.
ACCESSION  AA120437
VERSION     AA120437.1
KEYWORDS    EST.
SOURCE      house mouse.
ORGANISM    Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
REFERENCE  Merritt, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gibson, S., Kucher, L., Day, M., De, M., Martin, J., Morris, R.,
Shaw, J., Steward, R., Thompson, C., Treisman, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Matsuda, R.
The Mashu-BHVI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Mashu-BHVI Mouse EST Project of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNC, contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Ref: 321367 - 40m13.FT
Seq primer:
Location/Qualifiers
1. .50
/organism="Mus musculus"
/strain="C57BL/6 x DBA"
/db_xref="taxon:10090"
/clone="IMAGE:541052"
/culture="Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare top three leaves adult, heading
stage"
/dev_stage="adult"
/dev_stage="top three leaves"
/dev_stage="adult"
BASE COUNT      44 a      1 c      1 g      4 t
ORIGIN
Query Match      0.68: Score 24.4: DB 9: Length 50:
Best Local Similarity 68.08: Pval: NO 1.6e-06:
Matches 34: Conservative 0: Mismatches 16: Indels 0: Gaps 0:

OY 4218 AATGTTACAGCAAGCAATTAATGTCACCCACTTAATAAAAAAAAAA 4267
DB 1 AATGTTTAATAAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAA 50

RESULT 4
LOCUS      BF582680      45 bp      mRNA      linear      EST 12-DEC-2000
DEFINITION BF582680 602094085F1 NC1_CGAP_C024 Mus musculus cDNA clone IMAGE:4208373 5',
mRNA sequence.
ACCESSION  BF582680

```


ACCESSION	mRNA sequence.	
REF91166	BF691166.1 GI:11976574	
VERSION	1	
KEYWORDS	human.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) (bases 1 to 45)	
COMMENT	Email: cgaaps-f@mail.nih.gov Contact: Robert Struhsberg, Ph.D. Tissue Procurement: ATCC/DCDP/DP cDNA Library Preparation: ATCC/DCDP/DP cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Invivo Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://llnl198.llnl.gov: b column: 15 Plate: LCM1198 row: step: 45. Location/Qualifiers 1. .45 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_name="IMAGE:434369.5" /accession="AF043436.5" /feature_type="mammalian melanoma, high MOR" /lab_host="Dh10B (TI phage-resistant)" /note="Organ: skin; Vector: pMR-rtB (Clontech); Site_1: 5' (gccgcctccgcgcgc); Site_2: 5'fl (ggcctctatggcgc); Double-stranded cDNA was prepared from cell 1 line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-GACGCGCCATATGAGC-3' and 3' adaptor (where B = A, C, or G and N = A, C, G, or T) (30) average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 clones sequenced by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)." 7 c 4 g 4 t 30 a	
BASE COUNT	30 a 7 c 4 g 4 t	
ORIGIN		
Query Match	0.6%: Score 23.8; DB 12: Length 45;	
Best Local Similarity	72.1%: Pred. No. 2.1e-06;	
Matches 31: Conservative	0: Mismatches 12: Indels 0: Gaps 0:	
QY 4226	CAGACCAAAATTAATGTCAGCCACTTAAAAA 4268	
DB 2	CAGTACGCAAGATGTCTCAAAAAGAAAAA 44	
RESULT 13		
LOCUS	BF692288	
DEFINITION	mRNA sequence.	
VERSION	BF692288.1 GI:11976596	
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
SOURCE	human.	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) (bases 1 to 49)	
COMMENT	Email: cgaaps-f@mail.nih.gov Contact: Robert Struhsberg, Ph.D. Tissue Procurement: ATCC/DCDP/DP	

```

FEATURES
source
    cdna library Preparation: CLOUTERCH Laboratories, Inc.
    DNA Sequencing by: Inyte Genomics, Inc.
    Clone distribution: MCC clone distribution information can be
    found at: http://www.mcc.com/clone.htm
    http://image.dl.nsl.ac.g.e. Consortium/LINL.ac:
    Plate: LCMC1203 row: 1 column: 18
    High quality sequence stop: 49.
    Location/Qualifiers
        1..49
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="JIM.MCC.82"
            /type="cDNA"
            /map_peptide="melanotic melanoma, high MDR"
            /lab_host="DHIOB (T1 phage-resistant)"
            /note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
            Self (ggagcttcgagc); Site_2: SII (ggatcttcgagc);
            Double-stranded cDNA was prepared from cell lina RN.
            5' and 3' adaptors were used in cloning as follows: 5' adaptor
            sequence: GAGATATTGACGGCCCGGCGGCCTCAACTG-CT(30)RN3' adaptor
            (where B = A, C, or G and N = A, C, G, or T). Average
            insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
            contained inserts by PCR. This library was enriched for
            full-length clones and was constructed by Clontech
            Laboratories (Palo Alto, CA)."
BASE COUNT
31 a      6 c      6 g      6 t
ORIGIN
Paste Match
Best Match
Query Length 72.1nt; Score 23.8; DB 12; Length 49;
Local Similarity 72.1nt; Pred.No.2.le06;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0.
Cy 4226 CAGCACAAATAATATTCACCCACTTAATAAAAAAAAAAAAAA 4268
Db 2 CAGTACACCAACTGTCTCTCAAAAAAAAAAAAAAAAABBBBAAA 44
RESULT 14
LOCUS AU07269/C
DEFINITION AU07269 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
FEATURES
VERSION AU07269.1
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eularchia; Primates; Catarrhini; Hominoidei; Homin;
Individual: JIM.MCC.82; Tissue: Skin; Cell Type: Melanocytes;
Suzuki.Y., Takah.H., Tanoda.T., Mizushima-Sugano.J., Sase,J., Ihara
Y., Ota.T., Isogai.T., Tanaka,T., Morishima.S., Okubo.K., Sakaki
Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (3), 388-393 (2001)
JOURNAL 2127072
COMMENT Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Virology
4-6-1, Shirokandai, Minato-ku, Tokyo 106-8539, Japan
Email: shizuka@ems.u-tokyo.ac.jp
S. Construction and Characterization of a Full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library."

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```

BASP COUNT      /note="Differential display comparison of untreated and
                  dimethylformate treated U937 cells"
ORIGIN           8 a      18 c      7 g      17 t

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Query Match      0.6%; Score 23.8; DB 9; Length 50;
Best Local Similarity 72.1%; Pred. No. 2.1e+06;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 842 GGTGGCTGAAAGGAGAGAGTTTAAGCAGACGACATCGCAT 884
      | | | | | | | | | | | | | | | | | | | | | |
Db 46 GTTGGCTGAAAGGAGAGAGTCTCTGAGAGGCTAAGAGCAT 4

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```

RESULT 15
LOCUS      AU107270/c      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION AU107270 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION  AU107270      mRNA sequence.
VERSION     AU107270.1 GI:13556791
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens

```

```

REFERENCE   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.

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TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO REP. 2 (5), 388-393 (2001)

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COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp

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FEATURES
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
            1..50
            source

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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="LUNG9789"
            /clone_id="Sugano Homo sapiens cDNA library"
            /note="Differential display comparison of untreated and
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BASP COUNT      8 a      18 c      7 g      17 t
ORIGIN

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Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Cy 842 GGTGGCTGAAAGGAGAGAGTTTAAGCAGACGACATCGCAT 884
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Db 46 GTTGGCTGAAAGGAGAGAGTCTCTGAGAGGCTAAGAGCAT 4

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Search completed: December 11, 2002, 20:49:10
Job time : 3684 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: December 11, 2002, 16:33:52 : Search time 7159 Seconds
(without alignments)
17350.297 Million cell updates/sec

Title: US-09-954-556-3
Perfect score: 4268
Sequence: 1 cccaaggeccactctctgc.....acttaaaaaaaaaaaaaa 4268

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb.htg.*
3: gb.in.*
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8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.vi.*
14: gb.vi.*
15: en.ba.*
16: en.fun.*
17: en.hum.*
18: en.in.*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	30	0.7	30	6	I32954	I32954 Sequence 18
C 3	30	0.7	30	6	I87104	I87104 Sequence 18
C 4	27.4	0.6	36	9	S41355S1	S41355 BEX-fibrobl
C 5	27.4	0.6	36	9	S41355S1	S41355 BEX-fibrobl
C 6	25.8	0.6	30	6	A23008	A23008 DNA proc f
C 7	25.8	0.6	30	6	A23008	A23008 DNA proc f
C 8	25.8	0.6	30	6	A23008	A23008 DNA proc f
C 9	25.8	0.6	30	6	A23008	A23008 DNA proc f
C 10	25.8	0.6	30	6	A23008	A23008 DNA proc f
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C 23	25.8	0.6	30	6	A23008	A23008 DNA proc f
C 24	25.8	0.6	30	6	A23008	A23008 DNA proc f
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C 33	25.8	0.6	30	6	A23008	A23008 DNA proc f
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C 37	25.8	0.6	30	6	A23008	A23008 DNA proc f
C 38	25.8	0.6	30	6	A23008	A23008 DNA proc f
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C 40	25.8	0.6	30	6	A23008	A23008 DNA proc f
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ALIGNMENTS

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LOCUS AR007163 Sequence 15 from patent US 5750371. 39 bp DNA linear PAT 04-DEC-1998
DEFINITION AR007163 Sequence 15 from patent US 5750371.
ACCESSION AR007163
VERSION AR007163.1 GI:3966647
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 39)
AUTHORS Senoo M., Watanabe T. and Igarashi, K.
TITLE Water-soluble nuclein of RGF receptor, DNA and production thereof
JOURNAL Patent: US 5750371-A 15 12-MAY-1998;
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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BASE COUNT 7 a 11 c 2 g 16 t 3 others
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Best Local Similarity 84.6%; Pred. No. 4.6e+03;
Matches 33; Conservative 3; Mismatches 0; Gaps 0;

Qy 1873 GAGATGAGATGATGATGATGATGGAACACACAGCAAT 1911
DB 39 GATATGAGATGATGATGATGATGCGAGCATGAGAT 1

RESULT 2 >
LOCUS 132954/c 132954 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 15 from patent US 5589451.
VERSION 132954 132954 1
KEYWORDS 132954.1 GI:1823745
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wilson,S.E.
TITLE Methods and treatments for corneal healing with hepatocyte and
JOURNAL Patent: US 5589451-A 15 31-DEC-1996;
FEATURES
Location/Qualifiers
source 1. .30
BASE COUNT 11 a 7 c 4 g 8 t
ORIGIN

Query Match
Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1242 GATTGAGGTTCTCTATATTCGGAATGTAAAC 1271
DB 30 GATTGAGGTTCTCTATATTCGGAATGTAAAC 1

RESULT 3;
187104/c
LOCUS I87104 30 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 18 from patent US 5703047.
ACCESSION I87104
VERSION 187104.1 GI:3206822
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wilson,S.E.
TITLE Methods and treatments for corneal healing with growth factors
JOURNAL Patent: US 5703047-A 18 30-DEC-1997;
FEATURES
Location/Qualifiers
source 1. .30
BASE COUNT 11 a 7 c 4 g 8 t
ORIGIN

Query Match
Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
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DB 30 GATTGAGGTTCTCTATATTCGGAATGTAAAC 1

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source
1. .36
BASE COUNT 13 a 9 c 5 g 9 t
ORIGIN

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Score 27.4; DB 9; Length 36;
Best Local Similarity 96.6%; Pred. No. 1.1e+05;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2549 GAATTCCTCACTCTCACAACCAATGAGGA 2577
DB 1 GAATTCCTCACTCTCACAACCAATGAGGA 29

RESULT 5
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LOCUS S413551 36 bp DNA linear PRI 09-MAY-2000
DEFINITION TK25-fibroblast growth factor receptor [3' region] [human, normal
leukocyte DNA, Genomic, 36 nt, segment 1 of 2].
ACCESSION S413551
VERSION S41355.1 GI:232802
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens normal leukocyte DNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 36)
AUTHORS Champion-Arnaud,P., Ronsin,C., Gilbert,E., Gesnel,M.C.,
Houssaint,E. and Breathnach,R.
TITLE Multiple mRNAs code for proteins related to the BEK fibroblast
JOURNAL growth factor receptor
MEDLINE Oncogene 6 (6), 979-987 (1991)
PUBMED 1648704
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gbbseq 41845] from the original journal article.
This sequence comes from Fig. 4b.
FEATURES
source 1. .36
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="leukocyte"
BASE COUNT 13 a 9 c 5 g 9 t
ORIGIN

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LOCUS S418451 36 bp DNA linear PRI 09-MAY-2000
DEFINITION TK25-fibroblast growth factor receptor [3' region] [human, normal
leukocyte DNA, Genomic, 36 nt, segment 1 of 2].
ACCESSION S41845
VERSION S41845.1 GI:232806
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens normal leukocyte DNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 36)
AUTHORS Champion-Arnaud,P., Ronsin,C., Gilbert,E., Gesnel,M.C.,
Houssaint,E. and Breathnach,R.
TITLE Multiple mRNAs code for proteins related to the BEK fibroblast
JOURNAL growth factor receptor
MEDLINE Oncogene 6 (6), 979-987 (1991)
PUBMED 1648704
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gbbseq 41845] from the original journal article.
This sequence comes from Fig. 4b.
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Location/Qualifiers
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BASE COUNT 13 a 9 c 5 g 9 t
ORIGIN

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TITLE      Methods of assaying differential expression
JOURNAL    Patent: US 594076-A 431 30-NOV-1999;
FEATURES   Location/Qualifiers
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             1..25
             /organism="unknown"
BASE COUNT      3 a 10 c 7 g 5 t
ORIGIN

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Db	1	GCCTCCATGCTGCTGTCGGCGCCAAAC	25		
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LOCUS	AR090312	25 bp	DNA	linear	
DEFINITION	Sequence 432 from patent US 5994076..				
ACCESSION	AR090312				
VERSION	AR090312.1	GI:10017067			
KEYWORDS					

ORGANISM	UNKNOWN.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 25)
TITLE	Chenchi, A., Johadze, G. and Bibilashvili, R.
JOURNAL	Methods of assaying differential expression
FEATURES	Patent: US 594076-A 432 30-NOV-1999;
	Location/Qualifiers
	1 35
SOURCE	1

BASE COUNT		3	4	7	c	11	g	4	t
Query Match 0.5%; Score 25; DB 6; Length 25; Seq. Local Similarity 100.0%; Pred. No. 3.de-05; Matches 25; Conservative 0; Mismatches 0; Indels									
Qy	1179	CCCCGACGGGCTGCCTACCTCAAG	1203						
Db	25	GCCCGACGGGCTGCCTACCTCAAG	1						
RESULT 10									
AR197346									
LOCUS: tstrc1									
Accession: AR197346.123									
Size: 25 bp									
Type: DNA									
Library: linear									

VERSION	ARI97346.1	GI:20247195			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1. Unpublished O 25				
AUTHORS	Chenchiuk A., Jokidze G. and Bibilachvilli, R.				
TITLE	Methods of assaying different expression				
JOURNAL	Patent: US 6352829-A 431 05-MAR-2002;				
FEATURES	Location/Qualifiers 1. .25				
source	/organism="unknown"				
BASE COUNT	3 a 10 c			5 t	
ORIGIN					

	Matches	25;	Conservative	0;	Mismatches	0;	Indels
Qy	768	GCTCCATGCTGTGCTGCGCCAAC	792				
Db	1	GCTCCATGCTGTGCTGCGCCAAC	25				

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RESULT 11
LOCUS AR197347/c 25 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 432 from patent US 6352829.
ACCESSION AR197347
VERSION AR197347.1 GI:20247196
KEYWORDS
SOURCE Unknown.
ORGANISM
  UNCLASSIFIED
  1 (bases 1 to 25)
AUTHORS Chenchik, A., Johhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 432 05-MAR-2002;
FEATURES
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    Best Local Similarity 100.0%; Pred. No. 3.8e+05;
    Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy 1179 GCGGACGCGCGCTGACCTCAAG 1203
  Db 25 GCGGACGCGCGCTGACCTCAAG 1

RESULT 12
LOCUS AX077808 37 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 9 from Patent WO0107627.
ACCESSION AX077808
VERSION AX077808.1 GI:13157671
KEYWORDS
  synthetic construct.
  synthetic construct.
  artificial sequences.
  1 (bases 1 to 37)
AUTHORS Eisen, A.
TITLE Drosophila recombination-associated protein and methods for use
JOURNAL Patent: WO 0107627-A 9 01-FEB-2001;
FEATURES
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  source 1..37
  /organism="synthetic construct"
  /note="potential mutagenic oligonucleotide"
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    Matches 28; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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  Db 3 ACAGTGTATTTCAGCATTCAGCCAGCAGAT 36

RESULT 13
LOCUS AX248879 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 958 from Patent WO0156800.
ACCESSION AX248879
VERSION AX248879.1 GI:15863502
KEYWORDS
  human.
  Homo sapiens
  ORIGIN
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
  AUTHORS
  JOURNAL
  WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
  Location/Qualifiers
  source 1..31
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  /db_xref="taxon:9606"
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    Matches 26; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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  Db 1 ACCGGCCCTCTCTGRCGGCGGCTGCCGC 31

RESULT 14
LOCUS AR019665 24 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 4 from patent US 5783683.
ACCESSION AR019665
VERSION AR019665.1 GI:3974779
KEYWORDS
  Unknown.
  ORGANISM
    Unclassified.
    1 (bases 1 to 24)
AUTHORS Morrison, R.S.
TITLE Antisense oligonucleotides which reduce expression of the FGFRI
JOURNAL Patent: US 5783683-A 4 21-JUL-1998;
FEATURES
  Location/Qualifiers
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  /organism="unknown"
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    Best Local Similarity 100.0%; Pred. No. 6.7e+05;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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  Db 1 AAGTGTGACAGTGGGATTAAGTTC 24

RESULT 15
LOCUS AX347734 42 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 84 from Patent WO0196584.
ACCESSION AX347734
VERSION AX347734.1 GI:18495577
KEYWORDS
  southern root-knot nematode.
  Meloidogyne incognita
  ORGANISM
    Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchilina;
    Tylenchoidea; Heteroderidae; Meloidogyneae; Meloidogyne.
    1 (bases 1 to 42)
AUTHORS Mushaghi, A.R., Taylor, C.G., Keltelson, J.S. and Broshkin, A.M.
TITLE Methods and methods for the control of nematodes
JOURNAL Patent: WO 0196584-A 84 20-DEC-2001;
FEATURES
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  /db_xref="taxon:6306"
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Matches 29; Conservative 0; Mismatches 9; - Indels 0; Gaps 0;
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Search completed: December 11, 2002, 19:47:34
Job time : 7169 secs

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Sequence Alignment

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132954
VERSION
132954.1 GI:1823745
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SOURCE
ORGANISM
UNKNOWN.
REFERENCE
Unclassified.
1 (bases 1 to 30)
AUTHORS
WILSON, S E
TITLE
Methods and treatments for corneal healing with hepatocyte and
keratinocyte growth factors
Patent: US 5589451-A 15 31-DEC-1996;
Location/Qualifiers
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Source
BASE COUNT
11 a 7 c 4 g 8 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 30 GATTCAGCTTCCTCATTCGGAATGTAC 1

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132954
DEFINITION
Accession 18 from patent US 5703047.
187104
VERSION
187104.1 GI:3206822
KEYWORDS
SOURCE
ORGANISM
UNKNOWN.
REFERENCE
Unclassified.
1 (bases 1 to 30)
AUTHORS
WILSON, S E
TITLE
Methods and treatments for corneal healing with growth factors
Patent: US 5703047-A 18 30-DEC-1997;
Location/Qualifiers
1..30
Source
BASE COUNT
11 a 7 c 4 g 8 t
ORIGIN

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0.7%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1242 GATTCAGCTTCCTCATTCGGAATGTAC 1271
DB 30 GATTCAGCTTCCTCATTCGGAATGTAC 1

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	ACCESSION	AR090312				
	VERSION	AR090312.1				
	KEYWORDS	GI:10017067				
	SOURCE	Unknown.				
	ORGANISM	Unknown.				
	REFERENCE	Unclassified.				
	AUTHORS	1 (bases 1 to 25)				
	METHODS	Chemich,A., Johndae,G. and Bishlavwill,I.R.				
	JOURNAL	Methods US 5997076 differential expression				
	PATENT:	US 5997076				
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	0; Caps	0; Gaps				
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DB	25	GCCGAGCGGCCTGCCACTCAG 1				

7

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